

OM protein - protein search, using sw model

Run on: August 13, 2004, 09:06:38 ; Search time 173.932 Seconds
(without alignments)
1250.845 Million cell updates/sec

Title: US-09-785-215-2
Perfect score: 4058
Sequence: 1 MLPGLALLLLAAWTARALEV.....KMQQNGYENPTYKFFEQMQN 770

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

aa 672-714
aa 700-714

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Match	Length			
1	4058	100.0	770	1	AAP94775	Aap94775 Novel amy
2	4058	100.0	770	2	AAR41546	Aar41546 Mutated A
3	4058	100.0	770	2	AAR63442	Aar63442 Amyloid p
4	4058	100.0	770	2	AAW40130	Aaw40130 Human APP
5	4058	100.0	770	2	AAW97996	Aaw97996 Human amy
6	4058	100.0	770	4	AAE11762	Aae11762 Human amy
7	4058	100.0	770	4	AAE10648	Aae10648 Human amy
8	4058	100.0	770	4	AAE06893	Aae06893 Human amy
9	4058	100.0	770	4	AAE02600	Aae02600 Human amy

10	4058	100.0	770	4	AAU06622	Aau06622	Human par
11	4058	100.0	770	5	ABG94279	Abg94279	Amyloid b
12	4058	100.0	770	5	ABB78609	Abb78609	Human APP
13	4058	100.0	770	5	ABG76936	Abg76936	Humanised
14	4058	100.0	770	5	AAG68317	Aag68317	Human amy
15	4058	100.0	770	5	ABG80591	Abg80591	Human amy
16	4058	100.0	770	5	ABG32723	Abg32723	Human amy
17	4058	100.0	770	6	ABP72693	Abp72693	Human amy
18	4058	100.0	770	6	ABR43902	Abr43902	Beta-amyl
19	4058	100.0	770	6	ABP97885	Abp97885	Amino aci
20	4058	100.0	770	6	ABR61931	Abr61931	Human amy
21	4058	100.0	772	4	AAU07223	Aau07223	Human bet
22	4058	100.0	772	4	AAE10650	Aae10650	Human amy
23	4058	100.0	772	4	AAE06895	Aae06895	Human amy
24	4058	100.0	772	4	AAE02602	Aae02602	Human amy
25	4058	100.0	772	4	AAU06624	Aau06624	Human Amy
26	4058	100.0	772	5	ABB78611	Abb78611	Human APP
27	4054	99.9	770	2	AAR62505	Aar62505	Amyloid p
28	4053	99.9	770	2	AAW19485	Aaw19485	APP770 mu
29	4053	99.9	770	2	AAW19482	Aaw19482	APP770 mu
30	4053	99.9	770	2	AAW19497	Aaw19497	APP770 mu
31	4053	99.9	770	2	AAW19500	Aaw19500	APP770 mu
32	4053	99.9	770	4	AAE06913	Aae06913	Human amy
33	4053	99.9	770	5	ABB78008	Abb78008	Amino aci
34	4050	99.8	770	4	AAE06912	Aae06912	Human amy
35	4047	99.7	768	5	AAU80959	Aau80959	Human amy
36	4047	99.7	770	2	AAW19491	Aaw19491	APP770 mu
37	4047	99.7	770	2	AAW19506	Aaw19506	APP770 mu
38	4046	99.7	770	2	AAR26340	Aar26340	APP770. 3
39	4046	99.7	770	2	AAW19488	Aaw19488	APP770 mu
40	4046	99.7	770	2	AAW19503	Aaw19503	APP770 mu
41	4039	99.5	770	2	AAR05717	Aar05717	NAP gene
42	3943.5	97.2	751	2	AAR10022	Aar10022	Beta-amyl
43	3943.5	97.2	751	2	AAR20328	Aar20328	Sequence
44	3943.5	97.2	751	2	AAU08615	Aay08615	Human bet
45	3943.5	97.2	751	2	AAU08605	Aay08605	Human bet

ALIGNMENTS

RESULT 1

AAP94775

ID AAP94775 standard; protein; 770 AA.

XX

AC AAP94775;

XX

DT 25-MAR-2003 (revised)

DT 05-JUL-1990 (first entry)

XX

DE Novel amyloid precursor protein (NAP).

XX

KW SPAP; amyloid precursor protein; dysbolism; INS76; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Active-site 289. .345
 FT /*tag= a
 FT /label= INS76
 XX
 PN EP304013-A.
 XX
 PD 22-FEB-1989.
 XX
 PF 16-AUG-1988; 88EP-00113283.
 XX
 PR 15-AUG-1987; 87JP-00203298.
 PR 21-AUG-1987; 87JP-00207995.
 PR 18-NOV-1987; 87JP-00291404.
 PR 11-DEC-1987; 87JP-00313228.
 PR 05-FEB-1988; 88JP-00025260.
 PR 10-FEB-1988; 88JP-00029366.
 PR 19-FEB-1988; 88JP-00037905.
 PR 25-MAY-1988; 88JP-00125660.
 XX
 PA (ASAH) ASahi KASEI KOGYO KK.
 XX
 PI Kitaguchi N, Takahashi Y, Tokushima Y, Itoh H;
 XX
 DR WPI; 1989-055458/08.
 DR N-PSDB; AAN91049.
 XX
 PT Human senile plaque amyloid precursor protein and DNA - used for study
 PT and diagnosis of dysbolism in the central nervous system.
 XX
 PS Disclosure; Page; 108pp; English.
 XX
 CC AA. sequence from 289 to 345 encodes INS76 which is claimed as a senile
 CC plaque amyloid precursor (SPAP), useful for diagnosis of dysbolism in the
 CC CNS such as senile dementia. (Updated on 25-MAR-2003 to correct PA
 CC field.)
 XX
 SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 6.3e-289;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240

Qy	241	EADDDDEDDGDEVEEEAEEPYYEATERTTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDGDEVEEEAEEPYYEATERTTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLKTTQEPLARD	360
Qy	361	PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAERQA	420
Db	361	PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDVLNMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDVLNMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 2

AAR41546

ID AAR41546 standard; protein; 770 AA.

XX

AC AAR41546;

XX

DT 25-MAR-2003 (revised)

DT 15-MAR-1994 (first entry)

XX

DE Mutated APP770 exon 17 protein fragment.

XX

KW Probe; mutation; exon 17; amyloid precursor protein; APP770;

KW substitution; progressive presenile dementia; Alzheimer's disease;

KW cerebral haemorrhage; cerebral amyloid angiopathy; 4 kD fragment;

KW blood vessels; brain parenchyma; assay; processing; plaque.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers


```

FT      Misc-difference 692
FT      /note= "Position of mutation which causes abnormal
FT      processing of APP770"
XX
PN      EP561087-A1.
XX
PD      22-SEP-1993.
XX
PF      20-MAR-1992;    92EP-00400771.
XX
PR      20-MAR-1992;    92EP-00400771.
XX
PA      (INNO-) INNOGENETICS NV SA.
XX
PI      Van Broeckhoven C,  Martin J,  Hendriks L,  Cras P;
XX
DR      WPI; 1993-296442/38.
DR      N-PSDB; AAQ48860.
XX
PT      New mutant form of beta-amyloid polypeptide - related to development of
PT      cerebral haemorrhage and Alzheimer's disease, also corresp. nucleic acid,
PT      vectors, host cells and antibodies.
XX
PS      Disclosure; Fig 4; 21pp; English.
XX
CC      This sequence is encoded by exon 17 of the amyloid precursor protein
CC      APP770. A mutation at position 2075 of the DNA sequence, a C>G
CC      substitution, causes the substitution of Ala for Gly at codon 692. This
CC      mutation has been detected in related patients with progressive presenile
CC      dementia (Alzheimer's disease) or cerebral haemorrhage due to cerebral
CC      amyloid angiopathy. It may be responsible for the deposition of a 4 kD
CC      proteolytic fragment of APP in blood vessel walls and brain parenchyma.
CC      Probes specific for the mutation (see also AAQ48858-59) can be used to
CC      assay mRNA encoding substances which cause abnormal processing of APP
CC      related to plaque formation, and to detect this specific mutation.
CC      (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ      Sequence 770 AA;

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Query Match      100.0%;  Score 4058;  DB 2;  Length 770;
Best Local Similarity 100.0%;  Pred. No. 6.3e-289;
Matches 770;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDSPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240

Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Db	361	PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTET	600
Db	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 3

AAR63442

ID AAR63442 standard; protein; 770 AA.

XX

AC AAR63442;

XX

DT 25-MAR-2003 (revised)

DT 30-JUN-1995 (first entry)

XX

DE Amyloid protein precursor APP.

XX

KW Amyloid protein precursor; APP; beta-amyloid protein; gelatinase A;
 KW progelatinase A; decomposing agent; prophylaxis; Alzheimer's disease.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 672..711

FT /note= "beta-AP 1-40 gelatinase A cleavage sites"
 FT Cleavage-site 687. .689
 FT /label= gelatinase A
 FT Cleavage-site 701. .702
 FT /label= gelatinase A
 FT Cleavage-site 705. .706
 FT /label= gelatinase A
 XX
 PN EP622079-A2.
 XX
 PD 02-NOV-1994.
 XX
 PF 25-APR-1994; 94EP-00302924.
 XX
 PR 27-APR-1993; 93JP-00122207.
 PR 25-FEB-1994; 94JP-00051133.
 XX
 PA (ORIY) ORIENTAL YEAST CO LTD.
 XX
 PI Miyazaki K;
 XX
 DR WPI; 1994-334379/42.
 XX
 PT Gelatinase A-contg. amyloid beta protein decomposing agent - useful for
 PT prophylaxis or treatment of Alzheimer's disease.
 XX
 PS Disclosure; Fig 1; 12pp; English.
 XX
 CC AAR63442 describes the amino acid sequence of the amyloid protein
 CC precursor (APP), from which beta amyloid protein is derived (APB). An APB
 CC decomposing agent having either gelatinase A, a limited decomposate of
 CC gelatinase A, or progelatinase A as an active ingredient was developed.
 CC This agent can be used in medicine for prophylaxis and for the treatment
 CC of Alzheimer's disease. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 6.3e-289;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240

Qy	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSLTET	600
Db	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEI SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEI SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 4

AAW40130

ID AAW40130 standard; protein; 770 AA.

XX

AC AAW40130;

XX

DT 03-JUN-1998 (first entry)

XX

DE Human APP770 protein.

XX

KW Amyloid-beta peptide; A-beta; beta-AP; senile plaque; angiopathy; brain;

KW membrane-spanning glycoprotein; beta-amyloid precursor protein; APP770;

KW chromosome 21; human; Alzheimers disease; AD; amyloid filament;

KW treatment; disease; Down's syndrome; hereditary cerebral haemorrhage.

XX

OS Homo sapiens.

XX

PN WO9748983-A1.

XX

PD 24-DEC-1997.

XX
PF 18-JUN-1997; 97WO-US010601.
XX
PR 18-JUN-1996; 96US-00665649.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
PI Citron M, Selkoe DJ, Seubert PA, Schenk D;
XX
DR WPI; 1998-063287/06.
DR N-PSDB; AAV10322.
XX
PT Identifying compounds that alter cellular production of amyloid-beta 42
PT fragment - in vitro or in transgenic animal models, potentially useful
PT for treatment of Alzheimer's and other amyloid deposition diseases.
XX
PS Disclosure; Fig 10; 86pp; English.
XX
CC This sequence represents the human beta-amyloid precursor protein APP770,
CC which is a membrane-spanning glycoprotein encoded by a gene on the long
CC arm of chromosome 21. A fragment of the APP protein is known as the
CC amyloid-beta peptide (A-beta), also known as the beta-AP peptide, which
CC forms the subunit of the amyloid filaments comprising senile (amyloid)
CC plaques and the amyloid deposits in small cerebral and meningeal blood
CC vessels (amyloid angiopathy). The A-beta peptide can be a 39-43 amino
CC acid fragment. This invention provides methods of screening compounds for
CC their ability to alter the production of the A-beta peptide, which is
CC composed of >41 amino acids, alone, or in combination with the A-beta
CC peptide composed of 40 amino acids or less. Such agents that reduce the
CC production of the A-beta peptide are potentially useful for treatment of
CC Alzheimers Disease or other diseases involving amyloid deposition such as
CC Down's syndrome, hereditary cerebral haemorrhage with amyloidosis of
CC Dutch type and advanced aging of the brain
XX
SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.3e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVVEVAEEEEVAEVEEEE	240

Qy	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTET	600
Db	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN	770
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN	770

RESULT 5

AAW97996

ID AAW97996 standard; protein; 770 AA.

XX

AC AAW97996;

XX

DT 21-JUN-1999 (first entry)

XX

DE Human amyloid precursor protein.

XX

KW Amyloid precursor protein; APP; human; gene targetting;

KW homologous recombination; transgenic mouse; transgenic animal;

KW animal model; Alzheimer's disease.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 672..711

FT /note= "beta-amyloid domain"

XX

PN WO9909150-A1.
XX
PD 25-FEB-1999.
XX
PF 18-AUG-1997; 97WO-US014507.
XX
PR 18-AUG-1997; 97WO-US014507.
XX
PA (FARB) BAYER CORP.
XX
PI Wirak DO;
XX
DR WPI; 1999-181029/15.
XX
PT Modification of target nucleic acids - by homologous recombination, used
PT particularly for introducing a humanised amyloid precursor protein gene
PT into rodents for producing models of Alzheimer's disease.
XX
PS Disclosure; Page 85-88; 209pp; English.
XX
CC This polypeptide comprises human amyloid precursor protein (hAPP). The
CC invention provides a novel gene targetting strategy that facilitates the
CC introduction of one or more specific mutations into any gene in a single
CC double reciprocal homologous recombination step. The method has been used
CC particularly for introducing a humanised APP gene into rodents for
CC producing animal models of Alzheimer's disease (AD). 4 Independent lines
CC of transgenic mice (lines ES5007, ES5103, ES5401 and ES5403) have been
CC created using the novel gene targetting technique applied to embryonic
CC stem cells. In each line, the mouse APP gene was modified to encode a
CC mouse/human hybrid (m/hAPP) where amino acid residues 666-770 of APP770
CC are encoded by human cDNA sequences instead of mouse genomic exons (exons
CC 16-18). Within these residues, only 3 amino acid differences exist
CC between the mouse and human proteins, i.e. Gly-676 to Arg, Phe-681 to Thr
CC and Arg-684 to His. This exon-cDNA fusion gene therefore encodes an APP
CC containing a humanised beta-amyloid domain. Swedish, London,
CC Swedish/London and stop mutations have also been introduced. Targetting
CC vector sequences are provided (see AAX24730-33)
XX
SQ Sequence 770 AA;

Db	181		GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241		EADDDDEDEDGDEVEEEAEEPVEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241		EADDDDEDEDGDEVEEEAEEPVEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301		RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301		RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361		PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Db	361		PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Qy	421		KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421		KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481		QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481		QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541		MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTET	600
Db	541		MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTET	600
Qy	601		KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601		KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661		IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661		IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721		VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721		VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 6

AAE11762

ID AAE11762 standard; protein; 770 AA.

XX

AC AAE11762;

XX

DT 18-DEC-2001 (first entry)

XX

DE Human amyloid precursor protein (APP).

XX

KW Human; neuroprotective; nootropic; immunostimulant; Alzheimer's disease;

KW anticonvulsant; vaccine; gene therapy; Pick's disease; antidiabetic;

KW systemic amyloidosis; maturity onset diabetes; Parkinson's disease;

KW Huntington's disease; fronto-temporal dementia; encephalopathy; ALS;

KW amyotrophic lateral sclerosis; amyloid precursor protein; APP.

XX

OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Peptide 1. .18
 FT /label= Signal_peptide
 FT Domain 18. .700
 FT /label= Extracellular_domain
 FT Protein 19. .770
 FT /label= Mature_human_AAP_protein
 FT Region 672. .714
 FT /note= "Abeta-42/43 core peptide"
 FT Domain 700. .723
 FT /label= Transmembrane_domain
 FT Region 714. .770
 FT /note= "C-100 fragment"
 FT Domain 723. .770
 FT /label= Intracellular_domain
 XX
 PN WO200162284-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 19-FEB-2001; 2001WO-DK000113.
 XX
 PR 21-FEB-2000; 2000DK-00000265.
 PR 01-MAR-2000; 2000US-0186295P.
 XX
 PA (MEBI-) M & E BIOTECH AS.
 XX
 PI Birk P, Jensen MR, Nielsen KG;
 XX
 DR WPI; 2001-589796/66.
 DR N-PSDB; AAD18754.
 XX
 PT In vivo down-regulation of amyloid protein for the treatment of
 PT Alzheimer's, comprises presenting an amyloidogenic polypeptide or its
 PT subsequence and/or at least one analogue of the amyloidogenic polypeptide
 PT to the immune system.
 XX
 PS Claim 23; Page 113-116; 120pp; English.
 XX
 CC The invention relates to a method for in vivo down-regulation of amyloid
 CC protein such as beta amyloid (Abeta) in an animal, including human. The
 CC method comprising presenting to the animal's immune system an
 CC immunogenically effective amount of at least one amyloidogenic protein or
 CC its subsequence and/or at least one analogue of the amyloidogenic
 CC polypeptide. The amyloidogenic protein or its subsequence, and its
 CC analogue is useful for the preparation of an immunogenic composition
 CC comprising an adjuvant for down-regulating amyloid in an animal. They are
 CC also useful in the treatment, prophylaxis or amelioration of Alzheimer's
 CC disease or other diseases characterised by amyloid deposits. They are
 CC also useful in the treatment of systemic amyloidosis, maturity onset
 CC diabetes, Parkinson's disease, Huntington's disease, fronto-temporal
 CC dementia, amyotrophic lateral sclerosis (ALS), Pick's disease and prion-
 CC related transmissible spongiform encephalopathies. They are also useful
 CC for inducing production of antibodies against an amyloidogenic
 CC polypeptide. The present sequence is human amyloid precursor protein
 CC (APP)

XX

SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.3e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSTGK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSTGK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLOKEQNYSDDLANMISEPRISYGNLALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDELLOKEQNYSDDLANMISEPRISYGNLALMPSLTET	600
Qy	601	KTTVELLPVNGEFLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

Db 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

RESULT 7

AAE10648

ID AAE10648 standard; protein; 770 AA.

XX

AC AAE10648;

XX

DT 10-DEC-2001 (first entry)

XX

DE Human amyloid protein precursor 770 (APP770) isoform.

XX

KW Human; aspartyl protease 1; Aspl; amyloid precursor protein 770; APP770;

KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;

KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective.

XX

OS Homo sapiens.

XX

PN GB2357767-A.

XX

PD 04-JUL-2001.

XX

PF 22-SEP-2000; 2000GB-00023315.

XX

PR 23-SEP-1999; 99US-00404133.

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Bienkowski MJ, Gurney M;

XX

DR WPI; 2001-444208/48.

DR N-PSDB; AAD17897.

XX

PT Polypeptide comprising fragments of human aspartyl protease with amyloid

PT precursor protein processing activity and alpha-secretase activity, for

PT identifying modulators useful in treating Alzheimer's disease.

XX

PS Example 8; Page 142-144; 187pp; English.

XX

CC The patent discloses human aspartyl protease 1 (hu-Aspl) or modified Aspl

CC proteins which lack transmembrane domain or amino terminal domain or

CC cytoplasmic domain and retains alpha-secretase activity and amyloid

CC protein precursor (APP) processing activity. The proteins of the

CC invention are useful for assaying hu-Aspl alpha-secretase activity, which

CC in turn is useful for identifying modulators of hu-Aspl alpha-secretase

CC activity, where modulators that increase hu-Aspl alpha-secretase activity

CC are useful for treating Alzheimer's disease (AD) which causes progressive

CC dementia with consequent formation of amyloid plaques, neurofibrillary

CC tangles, gliosis and neuronal loss. Hu-Aspl protease substrate is useful

CC for assaying hu-Aspl proteolytic activity, by contacting hu-Aspl protein

CC with the substrate under acidic conditions and determining the level of

CC hu-Aspl proteolytic activity. The present sequence is amyloid protein

CC precursor 770 (APP770) isoform from human
XX
SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.3e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEEPVEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEEPVEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLOKEQNYSDVLNMISEPRISYGNDAIMPSTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDELLOKEQNYSDVLNMISEPRISYGNDAIMPSTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

|||||
Db 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

RESULT 8

AAE06893

ID AAE06893 standard; protein; 770 AA.

XX

AC AAE06893;

XX

DT 23-OCT-2001 (first entry)

XX

DE Human amyloid precursor protein 770 (APP770) isoform.

XX

KW Human; aspartyl protease; beta-amyloid precursor protein 770; APP770;

KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;

KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;

KW neuroprotective; antisense therapy; gene therapy; chromosome 21.

XX

OS Homo sapiens.

XX

PN WO200150829-A2.

XX

PD 19-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB000799.

XX

PR 09-MAY-2001; 2001WO-IB000799.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

XX

PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2001-483072/52.

DR N-PSDB; AAD13278.

XX

PT Novel purified polypeptide comprising fragment of mammalian aspartyl

PT protease 2, lacking Asp2 transmembrane domain and retaining beta

PT secretase activity of Asp2 useful for identifying inhibitors of Asp2

PT activity.

XX

PS Claim 8; Page 171-173; 185pp; English.

XX

CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.

CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. APP isoforms are useful for identifying

CC modulators of amyloid-beta peptide production, for use in designing

CC therapeutics for the treatment and prevention of Alzheimer's disease,

CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis

CC and neuronal loss. APP isoforms are also used in methods for identifying

CC inhibitors and modulators of human Asp2 activity. The invention relates

CC to a method for identifying agents that modulate the activity of human

CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta- and
CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting Hu-
CC Asp nucleic acids in in vitro assays and in Northern and Southern blots.
CC The present sequence is human wild-type amyloid precursor protein 770
CC (APP770) isoform. APP770 gene is localised of chromosome 21

XX

SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.3e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDDGDEVEEEAEEPVEEATERTTSIATTTTTTTESVEEVREVCSEQAETGPC	300
Db	241	EADDDDEDDGDEVEEEAEEPVEEATERTTSIATTTTTTTESVEEVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN	660

Qy 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 |||||
 Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
 |||||
 Db 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

RESULT 9

AAE02600

ID AAE02600 standard; protein; 770 AA.

XX

AC AAE02600;

XX

DT 10-AUG-2001 (first entry)

XX

DE Human amyloid precursor protein 770 (APP 770) protein.

XX

KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;

KW Alzheimer's disease; antialzheimer's.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 358

FT /note= "Encoded by GGC"

XX

PN WO200123533-A2.

XX

PD 05-APR-2001.

XX

PF 22-SEP-2000; 2000WO-US026080.

XX

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Gurney M, Bienkowski MJ;

XX

DR WPI; 2001-290516/30.

DR N-PSDB; AAD06770.

XX

PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
 PT protein, useful for the treatment of Alzheimer's disease.

XX

PS Example 8; Page 170-172; 189pp; English.

XX

CC The present invention relates to enzymes for cleaving the alpha-
 CC secretase site of the amyloid precursor protein (APP) and methods of
 CC identifying those enzymes. The methods may be used to identify enzymes
 CC that may be used to cleave the alpha-secretase cleavage site of the APP
 CC protein. The enzymes may be used to treat or modulate the progress of

CC Alzheimer's disease. The present sequence is human APP 770 protein
XX
SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.3e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEEPVEEATERTTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEEPVEEATERTTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

|||||
Db 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

RESULT 10

AAU06622

ID AAU06622 standard; protein; 770 AA.

XX

AC AAU06622;

XX

DT 24-OCT-2001 (first entry)

XX

DE Human partial Amyloid precursor protein, APP770.

XX

KW Human; Aspartyl protease; Asp2; beta-secretase; nootropic;

KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;

KW amyloid-beta; Abeta; APP770.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 358

FT /note= "Encoded by GCC"

XX

PN WO200149098-A2.

XX

PD 12-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB000798.

XX

PR 09-MAY-2001; 2001WO-IB000798.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

XX

PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2001-502549/55.

DR N-PSDB; AAS11549.

XX

PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.

XX

PS Disclosure; Page 171-173; 185pp; English.

XX

CC The invention relates to a purified polypeptide comprising a fragment of
CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC transmembrane domain and the Asp2 protein, and where the polypeptide and
CC the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. The invention also details polynucleotides for the Asp proteins
CC and vectors expressing them, and a polypeptide (isoform of amyloid
CC protein precursor (APP)) comprising the amino acid sequence of an APP or

CC its fragment containing an APP cleavage site recognizable by a mammalian
 CC beta-secretase, and further comprising two lysine residues at the
 CC carboxyl terminus of the amino acid sequence of the mammalian APP or APP
 CC fragment. Also included in the invention are methods of identifying
 CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
 CC useful for treating Alzheimer's disease. APP is useful in methods for
 CC identifying inhibitors or modulators of human Asp2 activity and amyloid-
 CC beta (Abeta) peptide production. APP is also useful in designing
 CC therapeutics for the treatment or prevention of Alzheimer's disease. APP
 CC comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is
 CC associated with increased levels of Abeta processing is useful in assays
 CC relating the Alzheimer's research. The expression vector is useful for
 CC recombinantly expressing APP. Nucleic acids that hybridise to Asp
 CC oligonucleotides are useful as probes or primers. The probes are useful
 CC for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and
 CC Southern blots. The present sequence is human APP770

XX

SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 4; Length 770;
 Best Local Similarity 100.0%; Pred. No. 6.3e-289;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540

Db 481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
 Qy 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRI SYGNDALMPSLTET 600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRI SYGNDALMPSLTET 600
 Qy 601 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 660
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 601 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 660
 Qy 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 Qy 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

RESULT 11

ABG94279

ID ABG94279 standard; protein; 770 AA.

XX

AC ABG94279;

XX

DT 10-DEC-2002 (first entry)

XX

DE Amyloid beta protein.

XX

KW Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
 KW cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
 KW vaccine; infectious disease.

XX

OS Homo sapiens.

XX

PN WO200256905-A2.

XX

PD 25-JUL-2002.

XX

PF 21-JAN-2002; 2002WO-IB000166.

XX

PR 19-JAN-2001; 2001US-0262379P.

PR 04-MAY-2001; 2001US-0288549P.

PR 05-OCT-2001; 2001US-0326998P.

PR 07-NOV-2001; 2001US-0331045P.

XX

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX

PI Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;
 PI Piossek C;

XX

DR WPI; 2002-627351/67.

XX

PT Molecular antigen array used in the production of vaccines for infectious
 PT diseases.

XX

PS Disclosure; Page 417-419; 441pp; English.

XX

CC This invention relates to a novel ordered and repetitive antigen array
CC used in the production of vaccines for infectious diseases. The invention
CC also discloses a composition comprising a non-natural molecular scaffold
CC comprising a core particle selected from a core particle of a non-natural
CC origin and a core particle of natural origin and an organiser comprising
CC at least one first attachment site, where the organiser is connected to
CC the core particle by at least one covalent bond. Also disclosed is an
CC antigen or antigenic determinant with at least one second attachment
CC site, where the antigen or antigenic determinant is amyloid beta peptide
CC (Abeta1-42) or its fragment and where the second attachment site is
CC selected from an attachment site not naturally occurring with the antigen
CC or antigenic determinant and an attachment site naturally occurring with
CC the antigen or antigenic determinant, where the second attachment site is
CC capable of association through at least one non-peptide bond to the first
CC attachment site and where the antigen or antigenic determinant and the
CC scaffold interact through the association to form an ordered and
CC repetitive antigen array. The invention also comprises a coat protein
CC capable of forming a capsid which comprises mutant Qbeta coat proteins
CC having an amino acid sequence selected from five amino acid sequences
CC fully defined in the specification. The compounds of the invention may
CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
CC immunisation and as a vaccine. The present sequence represents a protein
CC sequence used to create the compositions of the invention

XX

SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 5; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.3e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420

Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIHGHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 12

ABB78609

ID ABB78609 standard; protein; 770 AA.

XX

AC ABB78609;

XX

DT 16-JUL-2002 (first entry)

XX

DE Human APP770 protein sequence SEQ ID NO:55.

XX

KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic;
KW amyloid precursor protein; APP.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 358

FT /note= "encoded by GGC"

XX

PN GB2367060-A.

XX

PD 27-MAR-2002.

XX

PF 29-OCT-2001; 2001GB-00025934.

XX

PR 23-SEP-1999; 99US-00404133.

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.
PR 22-SEP-2000; 2000GB-00023315.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowski MJ, Gurney M;
XX
DR WPI; 2002-397167/43.
DR N-PSDB; ABL52489.
XX
PT Human aspartyl protease 1 substrates useful in assays to detect aspartyl
PT protease activity, e.g. for the diagnosis of Alzheimer's disease.
XX
PS Disclosure; Page 142-144; 182pp; English.
XX
CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC substrate (I) which comprises a peptide of no more than 50 amino acids,
CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC nucleotide sequence that hybridises under stringent conditions to the non
CC -coding strand complementary to a defined 1804 nucleotide sequence (see
CC ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1
CC proteolytic activity and lacks nucleotides encoding a transmembrane
CC domain); (3) a purified polynucleotide (III') comprising a sequence that
CC hybridises under stringent conditions to (III) (the nucleotide sequence
CC encodes a polypeptide further lacking a pro-peptide domain corresponding
CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC comprising (III) or (III'); and (5) a host cell (V) transformed or
CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC substrate (I) may be used as an enzyme substrate in assays to detect
CC aspartyl protease activity, (II) and therefore diagnose diseases
CC associated with aberrant hu-Asp1 expression and activity such as
CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC sequence represents human amyloid precursor protein APP770, which is used
CC in the exemplification of the present invention
XX
SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 5; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.3e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
QY	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
QY	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180

Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Db	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDVLNMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDVLNMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVVIAITVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVVIAITVIVITL	720
Qy	721	VMLKKKQYTSIIHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQRN	770
Db	721	VMLKKKQYTSIIHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQRN	770

RESULT 13

ABG76936

ID ABG76936 standard; protein; 770 AA.

XX

AC ABG76936;

XX

DT 05-NOV-2002 (first entry)

XX

DE Humanised antibody associated protein #5.

XX

KW Humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;

KW variable region complementarity determining region; 3D6; 10D5;

KW variable framework region; amyloidogenic disease; Alzheimer's disease;

KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;

KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;

KW Abeta; antibody.
 XX
 OS Homo sapiens.
 XX
 PN WO200246237-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 06-DEC-2001; 2001WO-US046587.
 XX
 PR 06-DEC-2000; 2000US-0251892P.
 XX
 PA (NEUR-) NEURALAB LTD.
 PA (AMHP) WYETH.
 XX
 PI Basi G, Saldanha J, Yednock T;
 XX
 DR WPI; 2002-519658/55.
 XX
 PT Novel light/heavy chain of humanized immunoglobulin for treating
 PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
 PT determining regions and variable framework region from human acceptor
 PT immunoglobulin.
 XX
 PS Disclosure; Page 165-167; 171pp; English.
 XX
 CC The present invention relates to new humanized immunoglobulin (Ig) light
 CC chain (LC) or heavy chain (HC) comprising variable region complementarity
 CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
 CC and variable framework region from human acceptor Ig LC or HC sequence.
 CC The invention is useful for preventing or treating an amyloidogenic
 CC disease or Alzheimer's disease in a patient. The invention is also useful
 CC for in vivo imaging amyloid deposits in a patient. The present amino acid
 CC sequence represents a humanized antibody associated protein as described
 CC in the invention
 XX
 SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 5; Length 770;
 Best Local Similarity 100.0%; Pred. No. 6.3e-289;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
QY	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
QY	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
QY	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240

Qy	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Db	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDVLNMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDVLNMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIIHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIIHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 14

AAG68317

ID AAG68317 standard; protein; 770 AA.

XX

AC AAG68317;

XX

DT 21-FEB-2002 (first entry)

XX

DE Human amyloid precursor protein (APP770) SEQ ID NO:5.

XX

KW Human; beta-amyloid; cyclin-dependent kinase inhibitor; nerve cell;
KW amyloid precursor protein; APP.

XX

OS Homo sapiens.

XX

PN WO200182967-A1.

XX

PD 08-NOV-2001.

XX

PF 25-APR-2001; 2001WO-JP003555.
 XX
 PR 28-APR-2000; 2000JP-00131037.
 XX
 PA (YAMA) YAMANOUCHI PHARM CO LTD.
 PA (SUZU/) SUZUKI T.
 XX
 PI Suzuki T, Watanabe T, Kawabata S, Hachiya S;
 XX
 DR WPI; 2002-026209/03.
 XX
 PT Medicinal compositions for the treatment of dementia and Alzheimer's
 PT disease, comprise compounds that suppress beta amyloid production.
 XX
 PS Disclosure; Page 39-42; 62pp; Japanese.
 XX
 CC The present invention describes medicinal compositions (I) inhibiting
 CC beta-amyloid production comprising an active component a substance that
 CC inhibits the activity of cyclin-dependent kinase (CDK). Also described
 CC are: (1) a method for screening compounds for their ability to inhibit
 CC the production of beta-amyloid by contacting with beta-amyloid producing
 CC cells; and (2) screening kits. (I) have nootropic and neuroprotective
 CC activities. (I) suppress the phosphorylation of amyloid precursor protein
 CC (APP) which is an essential step in the production of beta-amyloid. (I)
 CC can be used in the treatment and prevention of neurodegenerative diseases
 CC such as dementia and Alzheimer's disease. The present sequence represents
 CC the human APP770 protein which is used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 5; Length 770;
 Best Local Similarity 100.0%; Pred. No. 6.3e-289;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLKTTQEPLARD	360

Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 15

ABG80591

ID ABG80591 standard; protein; 770 AA.

XX

AC ABG80591;

XX

DT 29-NOV-2002 (first entry)

XX

DE Human amyloid beta protein.

XX

KW Molecular antigen array; vaccine; antigen; antimicrobial;

KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;

KW graft versus host disease; IgE-mediated allergic reaction; anaphylaxis;

KW adult respiratory distress syndrome; ARDS; Crohn's disease;

KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;

KW Grave's disease; systemic lupus erythematosus; osteoporosis;

KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;

KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;

KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;

KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;

KW enterokinase; cysteine-containing linker.

XX

OS Homo sapiens.

XX

PN WO200256907-A2.

XX

PD 25-JUL-2002.
 XX
 PF 21-JAN-2002; 2002WO-IB000168.
 XX
 PR 19-JAN-2001; 2001US-0262379P.
 PR 04-MAY-2001; 2001US-0288549P.
 PR 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR/) MAURER P.
 PA (LECH/) LECHNER F.
 PA (ORTM/) ORTMANN R.
 PA (LUEO/) LUEOEND R.
 PA (STAU/) STAUFENBIEL M.
 PA (FREY/) FREY P.
 XX
 PI Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;
 PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;
 XX
 DR WPI; 2002-636514/68.
 XX
 PT Molecular antigen array used in the production of vaccines for infectious
 PT diseases.
 XX
 PS Disclosure; Page 394-396; 418pp; English.
 XX
 CC The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an organiser comprising at least one first attachment
 CC site, where the organiser is connected to the core particle by at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site, where the antigen or antigenic determinant is
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
 CC attachment site is selected from: (i) an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; and (ii) an
 CC attachment site naturally occurring with the antigen or antigenic
 CC determinant, where the second attachment site is capable of association
 CC through at least one non-peptide bond to the first attachment site; and
 CC where the antigen or antigenic determinant and the scaffold interact
 CC through the association to form an ordered and repetitive antigen array.
 CC Also included is a process for producing a non-naturally occurring
 CC ordered and repetitive antigen array. The composition is used in
 CC immunisation and as a vaccine for diseases such as influenza, graft
 CC versus host disease, IgE-mediated allergic reactions, anaphylaxis, adult
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 CC gravis, immunoproliferative disease lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 CC osteoporosis and infectious diseases. The present sequence is an antigen
 CC for use in the array of the invention. The antigen is modified to possess
 CC a cleavage site (enterokinase or factor Xa) and a Cysteine- containing N-
 CC or C-terminal linker peptide which serves as the attachment point to a

CC virus like particle or bacterial protein (the scaffold protein)
XX
SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 5; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.3e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTESVEEVREVCSEAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTESVEEVREVCSEAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRI SYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRI SYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

Db |||||
721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

Search completed: August 13, 2004, 09:12:37
Job time : 178.932 secs

OM protein - protein search, using sw model

Run on: August 13, 2004, 09:09:23 ; Search time 52.6496 Seconds
 (without alignments)
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Title: US-09-785-215-2
 Perfect score: 4058
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Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	4058	100.0	770	1	US-08-133-248-8	Sequence 8, Appli
2	4058	100.0	770	1	US-08-231-940-1	Sequence 1, Appli
3	4058	100.0	770	2	US-08-641-774-1	Sequence 1, Appli
4	4058	100.0	770	2	US-08-104-165-3	Sequence 3, Appli
5	4058	100.0	770	3	US-08-464-250-3	Sequence 3, Appli
6	4058	100.0	770	4	US-08-464-250-3	Sequence 3, Appli
7	4058	100.0	770	4	US-09-548-372D-55	Sequence 55, Appl
8	4058	100.0	770	4	US-09-548-367D-55	Sequence 55, Appl
9	4058	100.0	770	4	US-09-551-853D-55	Sequence 55, Appl
10	4058	100.0	770	4	US-08-665-649-3	Sequence 3, Appli
11	4058	100.0	772	4	US-09-548-372D-59	Sequence 59, Appl

12	4058	100.0	772	4	US-09-548-367D-59	Sequence 59, Appl
13	4058	100.0	772	4	US-09-551-853D-59	Sequence 59, Appl
14	3943.5	97.2	751	1	US-08-123-702-4	Sequence 4, Appli
15	3943.5	97.2	751	2	US-08-104-165-2	Sequence 2, Appli
16	3943.5	97.2	751	2	US-08-422-333-2	Sequence 2, Appli
17	3943.5	97.2	751	2	US-08-422-333-21	Sequence 21, Appl
18	3943.5	97.2	751	3	US-08-464-250-2	Sequence 2, Appli
19	3943.5	97.2	751	4	US-08-464-250-2	Sequence 2, Appli
20	3943.5	97.2	751	4	US-08-832-867-5	Sequence 5, Appli
21	3943.5	97.2	751	4	US-09-548-372D-57	Sequence 57, Appl
22	3943.5	97.2	751	4	US-09-548-367D-57	Sequence 57, Appl
23	3943.5	97.2	751	4	US-09-551-853D-57	Sequence 57, Appl
24	3943.5	97.2	751	6	5187153-2	Patent No. 5187153
25	3943.5	97.2	751	6	5223482-2	Patent No. 5223482
26	3943.5	97.2	753	4	US-09-548-372D-61	Sequence 61, Appl
27	3943.5	97.2	753	4	US-09-548-367D-61	Sequence 61, Appl
28	3943.5	97.2	753	4	US-09-551-853D-61	Sequence 61, Appl
29	3937.5	97.0	751	6	5220013-2	Patent No. 5220013
30	3590.5	88.5	695	1	US-08-123-702-2	Sequence 2, Appli
31	3590.5	88.5	695	2	US-08-104-165-1	Sequence 1, Appli
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34	3590.5	88.5	695	4	US-09-458-481B-7	Sequence 7, Appli
35	3590.5	88.5	695	4	US-09-458-481B-8	Sequence 8, Appli
36	3590.5	88.5	695	4	US-09-548-372D-10	Sequence 10, Appl
37	3590.5	88.5	695	4	US-09-548-367D-10	Sequence 10, Appl
38	3590.5	88.5	695	4	US-09-551-853D-10	Sequence 10, Appl
39	3590.5	88.5	695	4	US-09-415-099-6	Sequence 6, Appli
40	3590.5	88.5	695	6	5218100-2	Patent No. 5218100
41	3590.5	88.5	697	4	US-09-548-372D-16	Sequence 16, Appl
42	3590.5	88.5	697	4	US-09-548-367D-16	Sequence 16, Appl
43	3590.5	88.5	697	4	US-09-551-853D-16	Sequence 16, Appl
44	3585.5	88.4	695	4	US-09-548-372D-14	Sequence 14, Appl
45	3585.5	88.4	695	4	US-09-548-367D-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-08-133-248-8

; Sequence 8, Application US/08133248

; Patent No. 5525714

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: MUTATED FORM OF THE BETA-AMYLOID PRECURSOR

; TITLE OF INVENTION: PROTEIN GENE

; NUMBER OF SEQUENCES: 8

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/133,248

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-133-248-8

Query Match 100.0%; Score 4058; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-263;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDPARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDPARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720

Qy 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQN 770
 |||||
 Db 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQN 770

RESULT 2

US-08-231-940-1
 ; Sequence 1, Application US/08231940
 ; Patent No. 5550216
 ; GENERAL INFORMATION:
 ; APPLICANT: MIYAZAKI, Kaoru
 ; TITLE OF INVENTION: GELATINASE A INHIBITOR
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/231,940
 ; FILING DATE: 25-APR-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 5-120457
 ; FILING DATE: 26-APR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 6-62129
 ; FILING DATE: 08-MAR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: NEIMARK, Sheridan
 ; REGISTRATION NUMBER: 20,520
 ; REFERENCE/DOCKET NUMBER: MIYAZAKI=4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; TELEX: 248633
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 770 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide

US-08-231-940-1

Query Match 100.0%; Score 4058; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 6e-263;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDAIMPSTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDAIMPSTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 3

US-08-641-774-1

; Sequence 1, Application US/08641774

; Patent No. 5843695

; GENERAL INFORMATION:

Db 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy 181 GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
 |||

Db 181 GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy 241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC 300
 |||

Db 241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC 300

Qy 301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360
 |||

Db 301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360

Qy 361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420
 |||

Db 361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420

Qy 421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
 |||

Db 421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480

Qy 481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
 |||

Db 481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTET 600
 |||

Db 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTET 600

Qy 601 KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 660
 |||

Db 601 KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 |||

Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQRN 770
 |||

Db 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQRN 770

RESULT 4

US-08-104-165-3

; Sequence 3, Application US/08104165

; Patent No. 5877015

; GENERAL INFORMATION:

; APPLICANT: HARDY, John Anthony

; APPLICANT: GOATE, Alison Mary

; APPLICANT: MULLAN, Michael John

; APPLICANT: CHARTIER-HARLIN, Marie-Christine

; APPLICANT: OWEN, Michael John

; TITLE OF INVENTION: Test and Model for Alzheimer's Disease

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Kourie and Crew

```

; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,165
; FILING DATE: 21-JAN-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9101307.8
; FILING DATE: 21-JAN-1991
; APPLICATION NUMBER: 9118445.7
; FILING DATE: 28-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16163-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-104-165-3

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Query Match          100.0%; Score 4058; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-263;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSTGK 60
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Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSTGK 60

QY     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

QY    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

QY    181 GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

QY    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC 300

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Qy 301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360
 |||||
 Db 301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360

Qy 361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420
 |||||
 Db 361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy 421 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
 |||||
 Db 421 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL 480

Qy 481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
 |||||
 Db 481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNLMPSLTET 600
 |||||
 Db 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNLMPSLTET 600

Qy 601 KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 660
 |||||
 Db 601 KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 |||||
 Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 770
 |||||
 Db 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 770

RESULT 5

US-08-464-250-3

; Sequence 3, Application US/08464250

; Patent No. 6107542

; GENERAL INFORMATION:

; APPLICANT: HARDY, John Anthony

; APPLICANT: GOATE, Alison Mary

; APPLICANT: MULLAN, Michael John

; APPLICANT: CHARTIER-HARLIN, Marie-Christine

; APPLICANT: OWEN, Michael John

; TITLE OF INVENTION: Test and Model for Alzheimer's Disease

; NUMBER OF SEQUENCES: .44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

Db 361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy 421 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
 |||

Db 421 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL 480

Qy 481 QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
 |||

Db 481 QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600
 |||

Db 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600

Qy 601 KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 660
 |||

Db 601 KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 |||

Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy 721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 770
 |||

Db 721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 770

RESULT 6

US-08-464-250-3

; Sequence 3, Application US/08464250

; Patent No. 6300540

; GENERAL INFORMATION:

; APPLICANT: HARDY, John Anthony

; GOATE, Alison Mary

; MULLAN, Michael John

; CHARTIER-HARLIN, Marie-Christine

; OWEN, Michael John

; TITLE OF INVENTION: Test and Model for Alzheimer's Disease

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Kourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/464,250

; FILING DATE: 05-Jun-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/104,165

; FILING DATE: 21-JAN-1992

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; APPLICATION NUMBER: 9101307.8
; FILING DATE: 21-JAN-1991
; APPLICATION NUMBER: 9118445.7
; FILING DATE: 28-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16163-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-464-250-3

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Query Match          100.0%; Score 4058; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-263;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
        |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
        |||
Db    181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy    241 EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC 300
        |||
Db    241 EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC 300

Qy    301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360
        |||
Db    301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360

Qy    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420
        |||
Db    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy    421 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQQLVETHMARVEAMLNDRRRLALENYITAL 480
        |||
Db    421 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQQLVETHMARVEAMLNDRRRLALENYITAL 480

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Qy 481 QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
 |||
 Db 481 QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSLTET 600
 |||
 Db 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSLTET 600

Qy 601 KTTVELLPVNGEFSDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 660
 |||
 Db 601 KTTVELLPVNGEFSDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 |||
 Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 770
 |||
 Db 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 770

RESULT 7

US-09-548-372D-55

; Sequence 55, Application US/09548372D

; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280I

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 55

; LENGTH: 770

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-548-372D-55

Query Match 100.0%; Score 4058; DB 4; Length 770;

Best Local Similarity 100.0%; Pred. No. 6e-263;

Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDS DPSGK 60
 |||
 Db 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDS DPSGK 60

Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDAIMPSTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDAIMPSTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 8

US-09-548-367D-55

; Sequence 55, Application US/09548367D

; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-55

Query Match 100.0%; Score 4058; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-263;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540

```

      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRVIYER 540

Qy      541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGN DALMPSLTET 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGN DALMPSLTET 600

Qy      601 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 660
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy      661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy      721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QN 770
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QN 770

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RESULT 9

US-09-551-853D-55

; Sequence 55, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D

; CURRENT FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 55

; LENGTH: 770

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-551-853D-55

Query Match 100.0%; Score 4058; DB 4; Length 770;

Best Local Similarity 100.0%; Pred. No. 6e-263;

Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy      61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

```


Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVREVCSEQAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRI SYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRI SYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAI IGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAI IGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 10

US-08-665-649-3

; Sequence 3, Application US/08665649

; Patent No. 6610493

; GENERAL INFORMATION:

; APPLICANT: CITRON, MARTIN

; APPLICANT: SELKOE, DENNIS J.

; APPLICANT: SEUBERT, PETER A.

; APPLICANT: SCHENK, DALE

```

; TITLE OF INVENTION: SCREENING COMPOUNDS FOR THE ABILITY TO
; TITLE OF INVENTION: ALTER THE PRODUCTION OF AMYLOID-BETA PEPTIDE (X-r41)
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,649
; FILING DATE: 18-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/437,067
; FILING DATE: 09-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: STORELLA ESQ., JOHN R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15270-000650
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-665-649-3

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Query Match          100.0%; Score 4058; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-263;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDS DPSG TK 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDS DPSG TK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLP CGIDKFR 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLP CGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

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Qy	241	EADDDDEDDDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 11

US-09-548-372D-59

; Sequence 59, Application US/09548372D

; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280I

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-59

Query Match 100.0%; Score 4058; DB 4; Length 772;
Best Local Similarity 100.0%; Pred. No. 6e-263;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEI SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720

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Db          |||||
661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy          721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMQN 770
          |||||
Db          721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMQN 770

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RESULT 12

US-09-548-367D-59

; Sequence 59, Application US/09548367D

; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280H

; CURRENT APPLICATION NUMBER: US/09/548,367D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 59

; LENGTH: 772

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-548-367D-59

Query Match 100.0%; Score 4058; DB 4; Length 772;

Best Local Similarity 100.0%; Pred. No. 6e-263;

Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
          |||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy          61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
          |||||
Db          61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy          121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
          |||||
Db          121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy          181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
          |||||
Db          181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy          241 EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

```

Db	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDAIMPSTET	600
Db	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDAIMPSTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 13

US-09-551-853D-59

; Sequence 59, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D

; CURRENT FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-59

Query Match 100.0%; Score 4058; DB 4; Length 772;
Best Local Similarity 100.0%; Pred. No. 6e-263;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAENERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAAENERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720

Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA TVIVITL 720

Qy 721 VMLKKKQYTSIH HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
 |||

Db 721 VMLKKKQYTSIH HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

RESULT 14

US-08-123-702-4

; Sequence 4, Application US/08123702

; Patent No. 5604131

; GENERAL INFORMATION:

; APPLICANT: Wadsworth, Samuel

; APPLICANT: Snyder, Benjamin

; APPLICANT: Reddy, Vermuri, B.

; APPLICANT: Wei, Chamer

; TITLE OF INVENTION: A cDNA Genomic Hybrid Sequence Encoding APP770

; Patent No. 5604131

; TITLE OF INVENTION: Containing a Genomic DNA Insert of the KI and OX-2 Regions

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patrea L. Pabst

; STREET: 2800 One Atlantic Center

; STREET: 1201 West Peachtree Street

; CITY: Atlanta

; STATE: GA

; COUNTRY: USA

; ZIP: 30309-3450

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/123,702

; FILING DATE: 17-SEPT-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Pabst, Patrea L.

; REGISTRATION NUMBER: 31,284

; REFERENCE/DOCKET NUMBER: TSI121

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404)-873-8794

; TELEFAX: (404)-873-8795

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 751 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-123-702-4

Query Match 97.2%; Score 3943.5; DB 1; Length 751;

Best Local Similarity 97.4%; Pred. No. 2.6e-255;

Matches 750; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSA-----	344
Qy	361	PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
		:	
Db	345	---IPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	401
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	402	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	461
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	462	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	521
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET	600
Db	522	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET	581
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	582	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	641
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	642	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	701
Qy	721	VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQRN	770
Db	702	VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQRN	751

RESULT 15

US-08-104-165-2

; Sequence 2, Application US/08104165

; Patent No. 5877015

```

; GENERAL INFORMATION:
;   APPLICANT:  HARDY, John Anthony
;   APPLICANT:  GOATE, Alison Mary
;   APPLICANT:  MULLAN, Michael John
;   APPLICANT:  CHARTIER-HARLIN, Marie-Christine
;   APPLICANT:  OWEN, Michael John
;   TITLE OF INVENTION:  Test and Model for Alzheimer's Disease
;   NUMBER OF SEQUENCES:  44
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Townsend and Townsend Khourie and Crew
;     STREET:    379 Lytton Avenue
;     CITY:      Palo Alto
;     STATE:     California
;     COUNTRY:   US
;     ZIP:       94301
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy Disk
;     COMPUTER:     IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/104,165
;     FILING DATE:       21-JAN-1992
;     CLASSIFICATION:    435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  9101307.8
;     FILING DATE:       21-JAN-1991
;     APPLICATION NUMBER:  9118445.7
;     FILING DATE:       28-AUG-1991
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Liebeschuetz, Joe
;     REGISTRATION NUMBER:  37,505
;     REFERENCE/DOCKET NUMBER:  16163-000100
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (415) 326-2400
;     TELEFAX:   (415) 326-2422
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  751 amino acids
;       TYPE:    amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-104-165-2

```

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Query Match          97.2%;  Score 3943.5;  DB 2;  Length 751;
Best Local Similarity 97.4%;  Pred. No. 2.6e-255;
Matches 750;  Conservative 1;  Mismatches 0;  Indels 19;  Gaps 1;

```

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDS DPSG TK 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDS DPSG TK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

```

Db	121	 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLP CGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	 GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSA-----	344
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	345	: ---IPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	401
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	402	 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	461
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	462	 QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	521
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGN DALMPSLTET	600
Db	522	 MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGN DALMPSLTET	581
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	582	 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN	641
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	642	 IKTEEISEVKMDAEFRHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	701
Qy	721	VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFE QMQN	770
Db	702	 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFE QMQN	751

Search completed: August 13, 2004, 09:17:35
Job time : 55.6496 secs

OM protein - protein search, using sw model

Run on: August 13, 2004, 09:08:23 ; Search time 42.3077 Seconds
 (without alignments)
 1750.686 Million cell updates/sec

Title: US-09-785-215-2
 Perfect score: 4058
 Sequence: 1 MLPGLALLLLAAWTARALEV.....KMQQNGYENPTYKFFEQMQN 770

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_78:*
 1: pirl:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	4058	100.0	770	1	QRHUA4	Alzheimer's diseas	
2	3590.5	88.5	695	1	A49795	Alzheimer's diseas	
3	3493.5	86.1	695	2	S00550	Alzheimer's diseas	
4	3468.5	85.5	695	2	A27485	Alzheimer's diseas	
5	3403.5	83.9	747	2	JH0773	Alzheimer's diseas	
6	2446.5	60.3	484	4	A32761	hypothetical Alzhe	
7	1981.5	48.8	763	2	A49321	amyloid beta (A4)	
8	1971.5	48.6	765	2	S42880	amyloid precursor-	
9	1956.5	48.2	751	2	A49974	beta-amyloid precu	
10	1150.5	28.4	653	2	A46362	amyloid precursor-	
11	1112.5	27.4	511	2	JC1404	CDEI-box DNA-bindi	
12	785	19.3	686	2	T15795	hypothetical prote	
13	737.5	18.2	886	2	A32758	beta-amyloid-like	

14	706	17.4	246	2	S38344	CDEI-binding prote
15	501	12.3	100	2	A32282	Alzheimer's diseas
16	411	10.1	82	2	PQ0438	Alzheimer's diseas
17	403	9.9	76	2	S06678	Alzheimer's diseas
18	397	9.8	76	2	S03607	Alzheimer's diseas
19	383	9.4	76	2	S04855	Alzheimer's diseas
20	296.5	7.3	191	2	A35981	sperm membrane pro
21	283	7.0	57	2	E60045	Alzheimer's diseas
22	283	7.0	57	2	F60045	Alzheimer's diseas
23	283	7.0	57	2	G60045	Alzheimer's diseas
24	283	7.0	57	2	D60045	Alzheimer's diseas
25	283	7.0	57	2	A60045	Alzheimer's diseas
26	283	7.0	57	2	B60045	Alzheimer's diseas
27	256.5	6.3	111	2	S41082	amyloid precursor
28	217	5.3	42	2	PN0512	beta-amyloid prote
29	194.5	4.8	2225	2	T26063	hypothetical prote
30	186	4.6	993	2	S49461	synaptonemal compl
31	183.5	4.5	396	2	S53325	tissue factor path
32	183	4.5	1188	2	T46608	zinc finger protei
33	179.5	4.4	1208	2	T27822	hypothetical prote
34	178.5	4.4	1110	2	I51116	NF-180 - sea lampr
35	177.5	4.4	2167	2	T34395	hypothetical prote
36	176.5	4.3	252	2	JG0185	hepatocyte growth
37	176	4.3	55	2	S30332	proteinase inhibit
38	175.5	4.3	579	2	JH0820	160K golgi antigen
39	175	4.3	302	1	TIRTGK	tissue factor path
40	175	4.3	1182	2	T30189	myelin transcripti
41	174.5	4.3	1271	2	A45555	glutamate rich pro
42	173.5	4.3	1087	2	T30330	gelsolin-related p
43	173.5	4.3	1558	2	C89114	protein C37C3.6a [
44	172	4.2	922	2	T23573	hypothetical prote
45	170.5	4.2	5170	2	T15348	hypothetical prote

ALIGNMENTS

RESULT 1

QRHUA4

Alzheimer's disease amyloid beta protein precursor [validated] - human

N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibitor; proteinase nexin II (PN-II)

N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular form; amyloid protein precursor splice form APP(695); amyloid protein precursor splice form APP(751); amyloid protein precursor splice form APP(770)

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000

C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44017; B44017; A03134; A29030; A47584; A47585; S02638; S00707; S00925; A38949; A30320; B30320; C30320; A31087; A24668; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252; S32539; S48148; S48692; S51186; S51185; S51184; S51183; A54238; I58075; I52250; S09010; S10737; S24127; S43644

R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Beyreuther, K.; Mueller-Hill, B.

Nucleic Acids Res. 17, 517-522, 1989

A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons.

A;Reference number: S02260; MUID:89128427; PMID:2783775
 A;Accession: S02260
 A;Molecule type: DNA
 A;Residues: 1-288,'V',365-770 <LEM1>
 A;Cross-references: EMBL:X13466
 A;Note: alternative splice form APP(695)
 R;Lemaire, H.G.
 submitted to the EMBL Data Library, November 1988
 A;Reference number: S05194
 A;Accession: S05194
 A;Molecule type: DNA
 A;Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>
 A;Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
 A;Note: alternative splice form APP(695)
 R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989
 A;Title: Characterization of the 5'-end region and the first two exons of the
 beta-protein precursor gene.
 A;Reference number: A32277; MUID:89165870; PMID:2538123
 A;Accession: A32277
 A;Molecule type: DNA
 A;Residues: 1-75 <LAF>
 A;Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1;
 PID:g516074
 R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little,
 S.P.
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
 A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows
 similarity to soybean trypsin inhibitor.
 A;Reference number: A33260; MUID:89392030; PMID:2675837
 A;Accession: A33260
 A;Molecule type: DNA
 A;Residues: 656-737 <JOH>
 A;Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
 R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.;
 Frangione, B.
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in
 amyloid of hereditary cerebral hemorrhage, Dutch type: DNA and protein
 diagnostic assays.
 A;Reference number: A35486; MUID:90321244; PMID:2196878
 A;Accession: A35486
 A;Molecule type: DNA
 A;Residues: 672-710 <PRE1>
 A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
 R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 87, 257-263, 1990
 A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A;Reference number: I39451; MUID:90236318; PMID:2110105
 A;Accession: I39452
 A;Status: nucleic acid sequence not shown; translation not shown; translated
 from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-770 <YOS1>
 A;Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
 A;Accession: I39451

A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-530,'QWLMPVIPAFWEAKVGR' <YOS2>
 A;Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
 R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 102, 291-292, 1991
 A;Reference number: A59020; MUID:91340168; PMID:1908403
 A;Contents: annotation; erratum
 A;Note: revised physical map for reference I39451
 R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duinen, S.G.; Bots, G.T.; Luyendijk, W.; Frangione, B.
 Science 248, 1124-1126, 1990
 A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrhage, Dutch type.
 A;Reference number: I39453; MUID:90260663; PMID:2111584
 A;Accession: I39453
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 656-737 <LEV>
 A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
 A;Note: a mutation with 693-Gln is presented
 R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer's disease.
 A;Reference number: I59562; MUID:92022553; PMID:1925564
 A;Accession: I59562
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 689-716,'F',718-737 <MUR>
 A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
 R;Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson, L.; O'dahl, S.; Nemens, E.; White, J.A.; Sadovnick, A.D.; Ball, M.J.; Kaye, J.; Warren, A.; McInnis, M.; Antonarakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin, G.M.; Bird, T.D.; Schellenberg, G.D.
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the APP gene region.
 A;Reference number: A44017; MUID:93035397; PMID:1415269
 A;Accession: A44017
 A;Molecule type: DNA
 A;Residues: 687-692,'G',694-718 <KAM1>
 A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
 A;Experimental source: familial Alzheimer disease family SB
 A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
 A;Accession: B44017
 A;Molecule type: DNA
 A;Residues: 687-718 <KAM2>
 A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
 A;Experimental source: familial Alzheimer disease family LIT
 A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
 A;Note: this sequence has a silent mutation
 R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.; Multhaup, G.; Beyreuther, K.; Muller-Hill, B.
 Nature 325, 733-736, 1987

A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor.
 A;Reference number: A03134; MUID:87144572; PMID:2881207
 A;Accession: A03134
 A;Molecule type: mRNA
 A;Residues: 1-288,'V',365-770 <KAN>
 A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
 A;Note: alternative splice form APP(695)
 R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides.
 A;Reference number: A29030; MUID:87231971; PMID:3035574
 A;Accession: A29030
 A;Molecule type: mRNA
 A;Residues: 284-288,'V',365-646,'E',648-770 <ROB>
 A;Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
 A;Note: the authors translated the codon GAG for residue 647 as Asp
 R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987
 A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid of Alzheimer's disease.
 A;Reference number: A47584; MUID:87120328; PMID:3810169
 A;Accession: A47584
 A;Molecule type: mRNA
 A;Residues: 674-756,'S',758-770 <GOL>
 A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
 A;Experimental source: brain
 R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Keuren, M.L.; Patterson, D.; Pagan, S.; Kurnit, D.M.; Neve, R.L.
 Science 235, 880-884, 1987
 A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near the Alzheimer locus.
 A;Reference number: A47585; MUID:87120329; PMID:2949367
 A;Accession: A47585
 A;Molecule type: mRNA
 A;Residues: 674-703 <TAN1>
 A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
 R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mueller-Hill, B.; Masters, C.L.; Beyreuther, K.
 EMBO J. 7, 949-957, 1988
 A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 precursor of Alzheimer's disease.
 A;Reference number: S02638; MUID:88296437; PMID:2900137
 A;Accession: S02638
 A;Molecule type: mRNA
 A;Residues: 672-678 <DYR>
 R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve, R.L.
 Nature 331, 528-530, 1988
 A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associated with Alzheimer's disease.
 A;Reference number: S00707; MUID:88122640; PMID:2893290
 A;Accession: S00707
 A;Molecule type: mRNA
 A;Residues: 286-344,'I',365-366 <TAN2>
 A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612

A;Experimental source: promyelocytic leukemia cell line HL60
 A;Note: alternative splice form APP(751)
 R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.;
 Greenberg, B.; Davis, K.; Wallace, W.; Lieberburg, I.; Fuller, F.; Cordell, B.
 Nature 331, 525-527, 1988
 A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase
 inhibitors.
 A;Reference number: S00925; MUID:88122639; PMID:2893289
 A;Accession: S00925
 A;Molecule type: mRNA
 A;Residues: 1-344, 'I', 365-770 <PO2>
 A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1;
 PID:g28721
 A;Note: alternative splice form APP(751)
 R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
 Nature 331, 530-532, 1988
 A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease
 inhibitory activity.
 A;Reference number: A38949; MUID:88122641; PMID:2893291
 A;Accession: A38949
 A;Molecule type: mRNA
 A;Residues: 287-367 <KIT>
 A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
 A;Experimental source: glioblastoma cell line
 A;Note: alternative splice form APP(770)
 R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer,
 B.; Ashton, R.A.; Macq, A.F.; Maloteaux, J.M.; Blume, A.J.; Octave, J.N.
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of
 three patients with sporadic Alzheimer's disease.
 A;Reference number: A30320
 A;Accession: A30320
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 284-288, 'V', 365-770 <VIT1>
 A;Accession: B30320
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 122-288, 'V', 365-770 <VIT2>
 A;Accession: C30320
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 606-770 <VIT3>
 R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.;
 Marotta, C.A.
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
 A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 disease brain: coding and noncoding regions of the fetal precursor mRNA are
 expressed in the cortex.
 A;Reference number: A31087; MUID:88124954; PMID:2893379
 A;Accession: A31087
 A;Molecule type: mRNA
 A;Residues: 507-770 <ZAI>
 A;Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
 A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for
 residue 603 as Val, GTG for residue 604 as Glu, GAG for residue 605 as Leu, CTT

for residue 607 as Pro, CCC for residue 608 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 655 as Ser
A;Note: the cited Genbank accession number, J03594, is not in release 101.0
R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, K.

Query Match 100.0%; Score 4058; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.6e-210;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
        |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
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Db    181 GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy    241 EADDDDEDDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTTESVEEVVREVCSEAETGPC 300
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Db    241 EADDDDEDDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTTESVEEVVREVCSEAETGPC 300

Qy    301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360
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Db    301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360

Qy    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420
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Db    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy    421 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
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Db    421 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL 480

Qy    481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
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Db    481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy    541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRI SYGNDALMPSLTET 600
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Qy    601 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 660
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Db    601 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy    661 IKTEEI SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAI IGLMVGGVVIATVIVITL 720
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Qy 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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Db 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMON 770

RESULT 2

A49795

Alzheimer's disease amyloid beta protein precursor - crab-eating macaque

C;Species: *Macaca fascicularis* (crab-eating macaque)

C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999

C;Accession: A49795

R;Podlisny, M.B.; Tolan, D.R.; Selkoe, D.J.

Am. J. Pathol. 138, 1423-1435, 1991

A;Title: Homology of the amyloid beta protein precursor in monkey and human supports a primate model for beta amyloidosis in Alzheimer's disease.

A;Reference number: A49795; MUID:91273117; PMID:1905108

A;Accession: A49795

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-695 <POD>

A;Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing

Query Match 88.5%; Score 3590.5; DB 1; Length 695;
Best Local Similarity 90.1%; Pred. No. 5.5e-185;
Matches 694; Conservative 1; Mismatches 0; Indels 75; Gaps 1;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSTGK 60
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Db 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSTGK 60

Qy 61 TCIDTKEGILQYCQEVPPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db 61 TCIDTKEGILQYCQEVPPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLP CGIDKFR 180
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 Db 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLP CGIDKFR 180

Qy 181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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 Db 181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy 241 EADDDDEDDGDEVVEEEAEEPYYEATERTTSIATTTTTTTSVVEEVREVCSEQAETGPC 300
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Db 241 EADDDDEDDGDEVVEEEAEEPYYEATERTTSIATTTTTTTSVVEEVR----- 288

Qy 301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARD 360

Db 289 ----- 288

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Qy      361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420
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Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
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Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	406	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	465
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Db	466	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	525
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	526	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	585
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	586	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	645
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMQN	770
Db	646	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMQN	695

RESULT 3

S00550

Alzheimer's disease amyloid beta protein precursor - rat

N;Alternate names: beta-A4 amyloid protein

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999

C;Accession: S00550; A41245; A39820; S46251

R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.

EMBO J. 7, 1365-1370, 1988

A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.

A;Reference number: S00550; MUID:88312583; PMID:2900758

A;Accession: S00550

A;Molecule type: mRNA

A;Residues: 1-695 <SHI>

A;Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617

R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.

Science 241, 223-226, 1988

A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core protein.

A;Reference number: A41245; MUID:88264430; PMID:2968652

A;Accession: A41245

A;Molecule type: protein

A;Residues: 18-37,'X',39-40,'X',42-44 <SCH>

A;Note: evidence for heparan sulfate attachment

R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.

FEBS Lett. 349, 109-116, 1994

A;Title: The beta-A4 amyloid precursor protein binding to copper.

A;Reference number: S46251; MUID:94320627; PMID:7913895

A;Contents: annotation; copper binding sites

A;Note: rat peptides were isolated but not sequenced
R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of
rat brain.
A;Reference number: A39820; MUID:91217087; PMID:1673681
A;Accession: A39820
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
A;Experimental source: brain
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or
plaques is characteristic of both Alzheimer's disease and Down's syndrome.
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F;625-648/Domain: transmembrane #status predicted <TMM>

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Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
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Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVREVCSEQAETGPC	300
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Db	241	EAEDDEDVEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVR-----	288
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARD	360
Db	289	-----	288
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
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Db	289	---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	345
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Db	346	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRLALENYITAL	405
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	406	QAVPPRPHHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	465

Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET	600
Db	466	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET	525
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	526	KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN	585
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	586	IKTEEISEVKMDAEFGHDSGFVHRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	645
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	646	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	695

RESULT 4

A27485

Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse

N;Alternate names: proteinase nexin II

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999

C;Accession: A27485; S19727; I49485

R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.

Biochem. Biophys. Res. Commun. 149, 665-671, 1987

A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor.

A;Reference number: A27485; MUID:88106489; PMID:3322280

A;Accession: A27485

A;Molecule type: mRNA

A;Residues: 1-695 <YAM>

A;Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085

A;Experimental source: brain

R;de Strooper, B.; van Leuven, F.; van den Berghe, H.

Biochim. Biophys. Acta 1129, 141-143, 1991

A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer related to its human homolog than previously reported.

A;Reference number: S19727; MUID:92096458; PMID:1756177

A;Accession: S19727

A;Molecule type: mRNA

A;Residues: 1-210,'G',212-220,'S',222-396,'A',398-402,'T',404-448,'A',450-695 <STR>

A;Cross-references: EMBL:X59379

R;Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.

Gene 112, 189-195, 1992

A;Title: Positive and negative regulatory elements for the expression of the Alzheimer's disease amyloid precursor-encoding gene in mouse.

A;Reference number: I49485; MUID:92209998; PMID:1555768

A;Accession: I49485

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-19 <RES>

A;Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329

C;Genetics:

A;Map position: 16C3

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology

C;Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 85.5%; Score 3468.5; DB 2; Length 695;
Best Local Similarity 87.3%; Pred. No. 1.9e-178;
Matches 672; Conservative 6; Mismatches 17; Indels 75; Gaps 1;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    181 GVEFVCCPLAEESDSVDSADAEEEDSDVWWVGADTDYADGGEDKVVEVAEEEEVADVVEEE 240

Qy    241 EADDDDEDDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    241 EADDDDEDVEDGDEVEEEAEEPVEEATERTTSTATTTTTTTESVEEVVR----- 288

Qy    301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARD 360
Db    289 ----- 288

Qy    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345

Qy    421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLDLENYIAL 405

Qy    481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    406 QAVPPRPHHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKATQIRSQVMTHLRVIYER 465

Qy    541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRI SYGNDALMPSLTET 600
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRI SYGNDALMPSLTET 525

Qy    601 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 660
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    526 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585

Qy    661 IKTEEI SEVKMDAEFRHDSGYEVHHQKL VFFAEDVGSNKGAI IGLMVGGVVIATVIVITL 720
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    586 IKTEEI SEVKMDAEFGHDSGFEVRHQKL VFFAEDVGSNKGAI IGLMVGGVVIATVIVITL 645

Qy    721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
```

|||||
Db 646 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695

RESULT 5

JH0773

Alzheimer's disease amyloid beta protein precursor - African clawed frog

C;Species: Xenopus laevis (African clawed frog)

C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999

C;Accession: JH0773

R;Okado, H.; Okamoto, H.

Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992

A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental regulation of its gene expression.

A;Reference number: JH0773; MUID:93129227; PMID:1282805

A;Accession: JH0773

A;Molecule type: mRNA

A;Residues: 1-747 <OKA>

A;Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151

A;Experimental source: larva

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing; amyloid

F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 83.9%; Score 3403.5; DB 2; Length 747;
Best Local Similarity 85.2%; Pred. No. 6.2e-175;
Matches 645; Conservative 40; Mismatches 45; Indels 27; Gaps 5;

Qy	17	ALEVPTDGNAGLLAEPQIAMF-CGRLNMHMNVQNGKWDS	SDPSG	TKTCID	TKEGILQYCQE	75
Db	15	ALEVLVDGNGGLLAEPQIAMFSVARLN	MHMNVQNGKWETDVSG	---	CIGTKEGILQYCQE	71
Qy	76	VYPELQITNVVEANQPVTIQNWCKRGRKQCKTH	PHFVI	PYRCLVGEFVSDALLVPDKCKF		135
Db	72	VYPELQITNVVEANQPVTIQNWCKKGRKQCKSR	THIVVPYRCLVGEFVSDALLVPDKCKF			131
Qy	136	LHQERMDVCETHLHWHTVAKETCSEKSTNLHDY	GMLLPCGIDKFRGVEFVCCPLAEESDN			195
Db	132	LHQERMDICETHLHWHTVAKESCSEKSM	SLHEYGMLLPCGIDKFRGVEFVCCPSAEES	ES		191
Qy	196	VDSADAEEDDS	VDVWGGADTDYADGSEDKVVEVA	--	EEEEVAEVEEEEADDD	EDDEDGDE 253
Db	192	FDSADAEEDDCDVWGGADADYVDRSDD	KAVEAQPDEEEEVVEVEEEEETDDDED	--	DGDE	249
Qy	254	VEEEAE	EPYEEATERTTSIATTTTTTTESV	EEVVREVCSEQAETGPCRAMISR	WYFDVTE	313
Db	250	AEEEP	EEPYEEATERTTSIATTTTTTTESV	EEVVREVCSEQAETGPCRAMISR	WYYDVTE	309
Qy	314	GKCAPFFYGGCGGNRNNFDTEEY	CMVCGSAMSQSLLKTTQEPLAR	DPVKLP	TTAASTPD	373
Db	310	SKCAQFIYGGCGGNRNNFESDDY	CMVCGSV	-----	IPATAASTPD	350
Qy	374	AVDKYLETPGDENEHAHFQKAKER	LEAKHRERMSQVMREWE	EAE	RQAKNLPKADKKAVIQ	433
Db	351	AVDKYLENPNDENEHDFL	KAKERLEGKHREKMSEVMKEWE	EAE	RQAKNLPKADKKAVIQ	410

QY 140 RMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLP CGIDKFRGVEFVCCPLAEESDNVDSA 199
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 RMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLP CGIDKFRGVEFVCCPLAEESDNVDSA 120

Qy	200	DAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEEADDDDEDDGDEVEEEEAE	259
Db	121	DAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEEADDDDEDDGDEVEEEEAE	180
Qy	260	EPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPCRAMISRWFYFDVTEGKCAPF	319
Db	181	EPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPCRAMISRWFYFDVTEGKCAPF	240
Qy	320	FYGGCGGNRRNFDTEEYCMVCGSAMSQSLLKTTQEPLARDPVKLPTTAASTPDAVDKYL	379
Db	241	FYGGCGGNRRNFDTEEYCMVCGSA-----IPTTAASTPDAVDKYL	281
Qy	380	ETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKV	439
Db	282	ETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKV	341
Qy	440	ESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLKKYVR	499
Db	342	ESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLKKYVR	401
Qy	500	AEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVAEEIQ	559
Db	402	AEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVAEEIQ	461
Qy	560	DEV	562
Db	462	DEV	464

RESULT 7

A49321

amyloid beta (A4) homolog 2 precursor - human

N;Alternate names: CDEI-binding protein

C;Species: Homo sapiens (man)

C;Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999

C;Accession: A49321; S34644; S40519

R;Sprecher, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, F.; Norris, K.; Foster, D.C.

Biochemistry 32, 4481-4486, 1993

A;Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: evidence for a multigene family.

A;Reference number: A49321; MUID:93250009; PMID:8485127

A;Accession: A49321

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-763 <SPR>

A;Cross-references: GB:S60099; NID:g300168; PIDN:AAC60589.1; PID:g300169

A;Experimental source: placenta

A;Note: sequence extracted from NCBI backbone (NCBIN:131198, NCBIP:131199)

A;Note: expression was shown in placenta, brain, heart, lung, liver, and kidney

R;von der Kammer, H.; Klaudiny, J.; Hanes, J.; Scheit, K.H.

submitted to the EMBL Data Library, April 1993

A;Description: The human homologue of the murine CDEI binding protein is an amyloid precursor like protein.

A;Reference number: S34644

A;Accession: S34644

A;Molecule type: mRNA
A;Residues: 1-763 <VON>
A;Cross-references: EMBL:Z22572; NID:g394763; PIDN:CAA80295.1; PID:g394764
R;Wasco, W.; Gurubhagavatula, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.; Hyman, B.T.; Neve, R.L.; Tanzi, R.E.
Nature Genet. 5, 95-99, 1993
A;Title: Isolation and characterization of APLP2 encoding a homologue of the Alzheimer's associated amyloid beta protein precursor.
A;Reference number: S40519; MUID:94035131; PMID:8220435
A;Accession: S40519
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-763 <WAS>
A;Cross-references: GB:L27631; NID:g450391; PIDN:AAC41701.1; PID:g450392
C;Genetics:
A;Gene: GDB:APLP2; APPL2
A;Cross-references: GDB:139159; OMIM:104776
A;Map position: 11q23-11q25
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; transmembrane protein
F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 48.8%; Score 1981.5; DB 2; Length 763;
Best Local Similarity 50.4%; Pred. No. 9.7e-99;
Matches 408; Conservative 127; Mismatches 168; Indels 107; Gaps 21;

Qy	5	LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDS	56
		: : : :	
Db	15	LLLLLLVGLTAPALALAGYIEALAANAGTGFVAEAPQIAMFCGKLNMHVNIQTGKWE	74
Qy	57	SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR	116
		: : : :	
Db	75	TGTKSCFETKEEVLQYCQEMYPELQITNVMEANQRVSIDNWCRRDKKQCKS--RFVTPFK	132
Qy	117	CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI	176
		: : : :	
Db	133	CLVGEFVSDVLLVPEKCQFFHKERMEVCENHQHWHTVKEACLTQGMTLYSYGMLLPCGV	192
Qy	177	DKFRGVFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAE	236
		: : : : : : : :	
Db	193	DQFHGTEYVCCPQTKIIGSVSKEEEEEDEE-----EEEEDEEEDYDVYKSEFPTEAD	245
Qy	237	VEE--EEA--DDDEDDGDEVEEEAE-----EPYEEATERTTSIATTTTTTTTESVE	284
		: : : : : : : : : : :	
Db	246	LEDFTAAVDEDEDEEEGEEVVEDRDYYYDTFKGDDYNE--ENPTEPGSDGTMSDKEIT	303
Qy	285	EVVREVCSEQAETGPCRAMISRWFYDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSA	344
		: : : : :	
Db	304	HDVKAVCSQEAMTGPCRAVMRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMVCKAM	363
Qy	345	MSQSLLKTTQEPLARDPVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRE	404
		: : : :	
Db	364	I-----PPTPLPT-----NDVDVYFETSADDNEHARFQKAKEQLEIRHRN	403
Qy	405	RMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAM	464
		: : : : : : : :	

Db 404 RMDRVKKEWEEAELQAKNLPKAERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAM 463
 Qy 465 LNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAA 524
 |||||:|||||: |||: |||| : ||:|||| ||| ||:|:| |||: |||
 Db 464 LNDRRRMALENYLAALQSDPPRPHRILQALRRYVRAENKDRHLHTIRHYQHVLAVDPEKAA 523
 Qy 525 QIRSQVMTHLRVIYERMNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDVLANMISEP 584
 |:| ||||| || || ||||| || |||: |||: |||||: ||| :|
 Db 524 QMKSQVMTHLHVIEERRNQSLSLLYKVPYVAQEIQEEIDELLQEQR-----ADM---- 572
 Qy 585 RISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARP 644
 | :||| | :| | :| :| | || ||| :|
 Db 573 -----DQFTASISETPVDVR---VSSEES-EEIPPFHPF--HPFPALPENE----DTQP 616
 Qy 645 AADRGLTTRPGSGLTN-----IKTEE---ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVG 696
 : : |||: | || | :| :| | :| :||| || ||
 Db 617 ELYHPM--KKGSGVGEQDGGGLIGAEKVINSKNKVDENMVIDETLDV--KEMIFNAERVG 672
 Qy 697 S-----NKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGVEVD 739
 : |:|||:| | |||||:||||:|:|| :| ||: ||||
 Db 673 GLEERESVGPLREDFSLSSSALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVD 732
 Qy 740 AAVTPEERHLSKMQQNGYENPTYKFFEQMQ 769
 :||||||: ||| :|||||||: ||||
 Db 733 PMLTPEERHLNKMQNHYENPTYKYLEQMQ 762

RESULT 8

S42880

amyloid precursor-like protein - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Mar-1999

C;Accession: S42880; S47528

R;Sandbrink, R.; Masters, C.L.; Beyreuther, K.

submitted to the EMBL Data Library, March 1994

A;Description: Complete nucleotide and deduced amino acid sequence of rat amyloid precursor-like protein 2 (Aplp2/Apph): Two amino acids length difference to human and murine homologues.

A;Reference number: S42880

A;Accession: S42880

A;Molecule type: mRNA

A;Residues: 1-765 <SAN>

A;Cross-references: EMBL:X77934

R;Sandbrink, R.; Masters, C.L.; Beyreuther, K.

Biochim. Biophys. Acta 1219, 167-170, 1994

A;Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protein precursor-like protein 2 (APLP2/APPH): two amino acids length difference to human and murine homologues.

A;Reference number: S47528; MUID:94368849; PMID:8086458

A;Accession: S47528

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-765 <SA2>

A;Cross-references: EMBL:X77934

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing

F;312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 48.6%; Score 1971.5; DB 2; Length 765;
Best Local Similarity 49.7%; Pred. No. 3.3e-98;
Matches 401; Conservative 134; Mismatches 173; Indels 99; Gaps 20;

```
Qy      5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWSDP 56
      | :|||  || | :          |||  :|||||||:||||:|:| |||: ||
Db      15 LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPPD 74

Qy      57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
      :|||:|: ||| :|||||:|||||||:||||| | :||:| :|||:: | |||::
Db      75 TGTKSCLGTKEEVLYCQEIYPELQITNVMEANQPVNIDSWCRRDKKQCRS--HIVIPFK 132

Qy     117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
      ||||| |||||: |:| |||||:||| | |||| || | : | : |||||:
Db     133 CLVGEFVSDVLLVPENCQFFHQERMEVCEKHQRWHTVVKEACLTEGMTLYSYGMLLPCGV 192

Qy     177 DKFRGVVEFVCCPLAE--ESDNVDSADAEEDDSVWVGADTDYA-DGSEDKVVEVAEEEE 233
      |:| | |:||| : :||: | : ||:: : : ||| | || | :
Db     193 DQFHGTEYVCCPQTKVVDSDSTMSKEEEEEEEEE-----DEEDYALDKSEFPTEADLEDF 248

Qy     234 VAEVEEEEEADDDDEDEDGDEVEEEAEPEYEE-----ATERTTSIATTTTTTTTESVEEVV 287
      | :|:| ::|::|:|:| | : : | : | | : : | : : : |
Db     249 EAAADEDEDEEEEEEEEEEGEEVVEDRDYYYDSFKGDDYNEENPTEPSSDGTISDKEIAHDV 308

Qy     288 REVCSEQAETGPCRAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQ 347
      : |||::| |||||:| |||||::| | ||||| |||||:|:| ||||| : :
Db     309 KAVCSQEAMTGPCRAVMRWFYDLSKGKCVRFIYGGCGGNRNNFESEDYCMVCKTMI-- 366

Qy     348 SLLKTTQEPLARDPVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMS 407
      | ||| : || | || | :||| |||||:| | :|| | |
Db     367 -----PPTPLPT-----NDVDVYFETSADDNEHARFQKAKEQLEIRHRSRMD 408

Qy     408 QVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLND 467
      :| :||| |||||:|:| :||| | :||:|:|:|:|:|:|:|:|:|:|
Db     409 RVKKEWEEAELQAKNLPKAERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLND 468

Qy     468 RRRLALENYITALQAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIR 527
      |||:|||||: |||: |||| : |::||| ||| ||::|:| | |||:||||:
Db     469 RRRIALENYLAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMK 528

Qy     528 SQVMTHLRVIYERMNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDVLANMISEPRIS 587
      ||||| || || ||||| || ||:|:|:|:|:|:|:|:|:|:|
Db     529 SQVMTHLHVIEERRNQSLSLLYKVPYVAQEIQEEIDELLQEQR-----ADM----- 574

Qy     588 YGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAAD 647
      | | :| | | : | | :| | :| | | :| | | :|
Db     575 ---DQFTSSISENPVDVR---VSSEES-EEIPPFHPF--HPFPSLENE---DTQPELY 621

Qy     648 RGLTTRPGSGLTN-----IKTEE---ISEVKMDAEFRHDSGYEVHHQKLVEFFAEDVGS-- 697
      : : |||: | || | : ||| | :| :::| || | |
Db     622 HPM--KKGSGMAEQDGGGLIGAEKVINSKNKMMDENMVIDETLDV--KEMIFNAERVGGLE 677

Qy     698 -----NKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGVEVDAAV 742
      : |:|:| | |||||:||||:|:| | :| ||:| | :
Db     678 EEPDSVGPLREDFSLSSSALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVHPML 737
```

Qy 743 TPEERHLSKMQQNGYENPTYKFFEQMQ 769
 |||||:| | :||| | | : | | |
 Db 738 TPEERHLNKMQNHGYENPTYKYLEQMQ 764

RESULT 9

A49974

beta-amyloid precursor protein 2 homolog APLP2 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999

C;Accession: A49974

R;Slunt, H.H.; Thinakaran, G.; Von Koch, C.; Lo, A.C.; Tanzi, R.E.; Sisodia, S.S.

J. Biol. Chem. 269, 2637-2644, 1994

A;Title: Expression of a ubiquitous, cross-reactive homologue of the mouse beta-amyloid precursor protein (APP).

A;Reference number: A49974; MUID:94132029; PMID:8300594

A;Accession: A49974

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-751 <SLU>

A;Cross-references: GB:U15571; NID:g558467; PIDN:AAA50603.1; PID:g558468

A;Note: sequence extracted from NCBI backbone (NCBIP:144636)

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 48.2%; Score 1956.5; DB 2; Length 751;
 Best Local Similarity 49.3%; Pred. No. 2.1e-97;
 Matches 397; Conservative 130; Mismatches 169; Indels 109; Gaps 20;

Qy 5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDS DP 56
 | :| | | | | : | | | : | | | | | | | : | | | : | | | : | |
 Db 15 LLVLLLLGLTAPAAALAGYIEALANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWE PD 74

Qy 57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
 : | | : | : | | : | | | | : | | | | | : | | | | | : | | | : | | | :
 Db 75 TGTKSCLGTKEEVLYCQEIYPELQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK 132

Qy 117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGM L L P C G I 176
 | | | | | | | | | | | | : | | | | : | | | | | | | : | | | : | | | | | :
 Db 133 CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSYGM L L P C G V 192

Qy 177 DKFRGVEFVCCPLAE--ESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAE---E 231
 | : | | | : | | | : : | | : | : | | : : | | | | | : | | | : | | | :
 Db 193 DQFHGTEYVCCPQTKTVDS DSTMSKEEEEEEE-----DEEDEEEDYDL DKSEFPTE 243

Qy 232 EEVAEVEEEEEAD-DDEDDEDGDEVEEEAE-----EPYEEATERTTSIATTTT T T T T S 282
 : : : | | : : | | : | | : | | : : : | | | | | : | | | : | | : :
 Db 244 ADLEDFTEAAADEEEEEDEEEGEEVVEDRDYYYDPFKGDDYNE--ENPTEPSSEGTIS DKE 301

Qy 283 VEEVVREVCSEQAETGPCRAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCM AVCG 342
 : | : | | : : | | | | : : | | | : : | | | | | : : | | | | | :
 Db 302 IVHDVKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCM AVCK 361

Qy 343 SAMSQSLLKTTQEPLARDPVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKH 402

```

      : :      | |||      : || | || | :||| | |||||:| | :|
Db      362 AMI-----PPTPLPT-----NDVDVYFETSADDNEHARFQKAKEQLEIRH 401
Qy      403 RERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVE 462
      | || :| :||| | ||||| ::: :||| | |::|:| |:| |||||:| |||
Db      402 RNRMDRVKKEWEEAELQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVE 461
Qy      463 AMLNDRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPPK 522
      |||||:| |||: |||: ||| : |::| ||| || |::|:| | ||:|
Db      462 AMLNDRRIAENYLAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEK 521
Qy      523 AAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMIS 582
      ||::| ||||| || || ||||| || ||:| |:| |:| |:| |:| |:|
Db      522 AAQMKSQVMTHLHVIEERNQSLSLLYKVPYVAQEIQEEIDELLQEQR-----ADM-- 572
Qy      583 EPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDA 642
      | | |::| | : | : | | | | | : : |||
Db      573 -----DQFTSSISENPVDVRVSSEESE-EIPPFHPLHPF-----PSLSENE----- 612
Qy      643 RPAADRGLTTRPGSGLTNIKTEEI-SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS---- 697
      |: : | || : : | |: ||| | :| ::::| || ||
Db      613 ----GSGMAEQDG-GLIGAEKVINSKNKMMDENMVIDETLDV--KEMIFNAERVGGLEEE 665
Qy      698 -----NKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVEVDAAVTP 744
      : |::|:| | |||||:| |:| |:| |:| |:| |:|
Db      666 PESVGPLREDFSLSSNALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTP 725
Qy      745 EERHLSKMQQNGYENPTYKFFEQQM 769
      ||||:| | :||| |||: |||
Db      726 EERHLNKMQNHGYENPTYKYLEQQM 750

```

RESULT 10

A46362

amyloid precursor-like protein - mouse

C;Species: Mus musculus (house mouse)

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999

C;Accession: A46362

R;Wasco, W.; Bupp, K.; Magendantz, M.; Gusella, J.F.; Tanzi, R.E.; Solomon, F.
Proc. Natl. Acad. Sci. U.S.A. 89, 10758-10762, 1992

A;Title: Identification of a mouse brain cDNA that encodes a protein related to
the Alzheimer disease-associated amyloid beta protein precursor.

A;Reference number: A46362; MUID:93066322; PMID:1279693

A;Accession: A46362

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-653 <WAS>

A;Experimental source: brain

A;Note: sequence inconsistent with the nucleotide translation

A;Note: sequence extracted from NCBI backbone (NCBIN:118683, NCBIP:118684)

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology

C;Keywords: transmembrane protein

Query Match 28.4%; Score 1150.5; DB 2; Length 653;

Best Local Similarity 35.4%; Pred. No. 2.6e-54;

Matches 274; Conservative 120; Mismatches 228; Indels 153; Gaps 19;

Qy 1 MLPGGLALLLLAAWTARA-LEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGT 59
 :|| |:|||| | | : | |:| |||| :| ::| |:|: || :
 Db 22 LLP-LSLLLLRAQLAVGNLAVGSPSAAEAPGSAQVAGLCGRITLHRDLRTGRWEPDPQRS 80

Qy 60 KTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHF-VIPYRCL 118
 : |: : :|:|:|:|:| | | :| | : :| | | | | | |:|: ||
 Db 81 RRCLLDPQRVLEYCRQMYPELHIARVEQAAQAI PMERWCGGTRSGRCAHPHHEVVPFHCL 140

Qy 119 VGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDK 178
 |||||:|||||: |:| ||||| ||: | |:| || : || ||||| |:|
 Db 141 PGEFVSEALLVPEGCRFLHQERMDQCESSTRRHQEAQEACSSQGLILHGSGMMLPCGSDR 200

Qy 179 FRGVEFVCCPLAEESDNVDSADAEEDDSVW-WGGADTDYADGSEDKVVEVAEEEEVAEV 237
 |||||:|||| : | : : | || |:| || ||||
 Db 201 FRGVEYVCCP-PPATPNPSGMAAGDPSTRSWPLGGR----AEGGED-----EEEVESF 248

Qy 238 EEEEADDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAET 297
 : | : :| ||| || : |
 Db 249 PQPVDDYFVEPPQAEEEEEEEEEERAPPPSSHTP----- 281

Qy 298 GPCRAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPL 357
 |:|| ||
 Db 282 ----VMVSR----VT----- 288

Qy 358 ARDPVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAE 417
 | || | || | |: || |:| || : :::| |||| |:|
 Db 289 ---PTPRPT-----DGVDVYFGMPGEIGEHEGFLRAKMDLEERRMRQINEVMREWAMAD 339

Qy 418 RQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYI 477
 |:| |||||:|:|:| ||| :::|:|:| : |||:| || | |:|:| || ||| ::
 Db 340 SQSKNLPKADRQALNEHFQSILQTLQVSGERQRLVETHATRVLIALINDQRRAALEGFL 399

Qy 478 TALQAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVI 537
 ||| ||: | |:|:| |||||:|:|:| |:| || |:| || |||:| |
 Db 400 AALQGDPPQAERVLMLRRYLRAEQKEQRHTLRHYQHVAVDPEKAQQMRQVQVTHLQVI 459

Qy 538 YERMNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNLALMP-S 596
 ||||| || | :|:|:| :| || | : : | | :| |
 Db 460 EERMNQSLGLLDQNPFLAQELRPQIQELL-----LAEHLGPSEL----DASVPGS 505

Qy 597 LTETKTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGS 656
 :| | ||| |:|:| | :| | :| | :|
 Db 506 SSEDK-----GSLQP-----PESKDDPPVTLP---KGSTDQESS 536

Qy 657 GLTNIKTEEISEVKMDAEFRHDSGYEVHH---QKLVEFFAEDVGSNKGAIIGLMVGGVVIA 713
 | : : : |: | |: | : :| :|:| :|
 Db 537 SSGREKLTPLQYEQKVNASAPRGFPFHSSDIQRDELAPSGTGVSREALSGLLIMGAGGG 596

Qy 714 TVIVITLVML-KKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQ 767
 ::|:|:|:| ||| |:| ||||| :| ||:| :|:|:| |||||:| |:
 Db 597 SLIVLSLLLLRKKKPYGTISHGVVEVDPMLEEQQLRELQRHGYENPTYRFL 651

RESULT 11

JC1404

CDEI-box DNA-binding protein - mouse

C;Species: Mus musculus (house mouse)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997
 C;Accession: JC1404
 R;Vidal, F.; Blangy, A.; Rassoulzadegan, M.; Cuzin, F.
 Biochem. Biophys. Res. Commun. 189, 1336-1341, 1992
 A;Title: A murine sequence-specific DNA binding protein shows extensive local similarities to the amyloid precursor protein.
 A;Reference number: JC1404; MUID:93129193; PMID:1482349
 A;Accession: JC1404
 A;Molecule type: mRNA
 A;Residues: 1-511 <VID>
 C;Comment: This protein plays an important role in the early development of the mouse.
 C;Keywords: DNA binding; transmembrane protein

Query Match 27.4%; Score 1112.5; DB 2; Length 511;
 Best Local Similarity 43.0%; Pred. No. 2.1e-52;
 Matches 264; Conservative 87; Mismatches 136; Indels 127; Gaps 21;

QY	174	CGIDKFRGVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEE	233
		:: : :: :	
Db	6	CGVDQFHGTEYVCCP---QTKTVDS-----DSTMSK-----EEEE	37
QY	234	VAEVEEEEEADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSE	293
		: : : : : : : :	
Db	38	----EEDEEDEEEDYDLKSEFPTEADLEDFTE---AAADEEEEEEEGEEVVED----	86
QY	294	QAETGPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTT	353
		: : : : : : :	
Db	87	-----RDYYD-----PF----KGDDYNEENPTE-----PSSEGTI--S	114
QY	354	QEPLARDPVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREW	413
		: : :: : : : :	
Db	115	DKEIVHD-VKVPPTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKKEW	172
QY	414	EEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLAL	473
		::: : ::: : : : : : : : : : : : :	
Db	173	EEAELQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRIAL	232
QY	474	ENYITALQAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTH	533
		: : : :: :: : : : :	
Db	233	ENYLAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTH	292
QY	534	LRVIYERMNQSLSLLYNVPAAVEEIQDEVDELLQEQNYSDDLANMISEPRI SYGNDAL	593
		: : : : : : : : :	
Db	293	LHVIEERNQSLSLLYKVPYVAQEIQEEIDELLQEQR-----ADM-----DQF	335
QY	594	MPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTR	653
		:: : : : : : :	
Db	336	TSSISENPVDVRVSSESE-EIPPFHPLHPF-----PSLSENE-----GSGMAEQ	379
QY	654	PGSGLTNIKTEEI-SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS-----	697
		: : : : :::	
Db	380	DG-GLIGAEKVINSKNKM DENMVIDETLDV--KEMIFNAERVGGLEEEPE SVGPLREDF	436
QY	698	--NKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQN	755
		: : : : : : : : : : :	

Db 437 SLSSNALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNH 496
Qy 756 GYENPTYKFFEQMQ 769
|||||||: ||||
Db 497 GYENPTYKYLEQMQ 510

RESULT 12

T15795

hypothetical protein C42D8.8 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 01-Dec-2000

C;Accession: T15795; A49414

R;Hallsworth, K.

submitted to the EMBL Data Library, April 1996

A;Description: The sequence of C. elegans cosmid C42D8.

A;Reference number: Z18405

A;Accession: T15795

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-686 <HAL>

A;Cross-references: EMBL:U56966; NID:g1293844; PID:g1293850; PIDN:AAA98722.1;
GSPDB:GN00028; CESP:C42D8.8

A;Experimental source: strain Bristol N2; clone C42D8

R;Daigle, I.; Li, C.

Proc. Natl. Acad. Sci. U.S.A. 90, 12045-12049, 1993

A;Title: apl-1, a Caenorhabditis elegans gene encoding a protein related to the
human beta-amyloid protein precursor.

A;Reference number: A49414; MUID:94089766; PMID:8265668

A;Accession: A49414

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 7-686 <DAI>

A;Cross-references: GB:U00240; NID:g416296; PIDN:AAC46470.1; PID:g416297

C;Genetics:

A;Gene: CESP:C42D8.8

A;Map position: X

A;Introns: 22/3; 78/3; 121/1; 199/1; 230/1; 274/3; 344/3; 410/2; 471/2; 537/3;
580/3

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology

Query Match 19.3%; Score 785; DB 2; Length 686;

Best Local Similarity 26.8%; Pred. No. 1.1e-34;

Matches 224; Conservative 111; Mismatches 272; Indels 230; Gaps 23;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDS DPSG TK 60
:: || : :| | | | | :| || | :| : | | :|

Db 6 LMIGLLIPILVA-TVYAEGSPAGSKRHEKFIPMVAFSCGYRNQYM-TEEGSWKTDDERYA 63

Qy 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
|| | ||:|||| : || : |||:| : | :| :| : || | | | | : |

Db 64 TCFSGKLDILKYCRKAYPSMNITNIVEYSHEVSISDWCREEGSPCK-WTHSVRPYHCIDG 122

Qy 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTN-----LHDYGM LLP C 174
|| | :|| || | :| | | : || | : | | : : : | ||

Db 123 EFHSEALQVPHDCQFSHVNSRDQCNDYQHWKDEAGKQCKTKKSKGNKDMIVRSFAVLEPC 182

Qy 175 GIDKFRGVFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEV 234
 :| | | | | | | | :| : | ::
 Db 183 ALDMFTGVFVCCP----NDQTNKTDVQKTK----- 209

Qy 235 AEVEEEEADDDDEDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEQ 294
 |:|: | | | | | | |: | |::| | |
 Db 210 ---EDEDDDDDDEDDAYEDDYSEESDEKDEE----- 236

Qy 295 AETGPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQ 354
 Db 237 ----- 236

Qy 355 EPLARDPVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWE 414
 || ::|| | : || | :||: |:| :||::: |:|:| |
 Db 237 EPSSQDP-----YFKIANWTNEHDDFKKAEMRMDEKHKVVDKVMKEWG 280

Qy 415 EA-----ERQAKNLPKADKKAVIQ---HFQEKVESLEQEAANERQQLVETHMARVEAMLN 466
 : |::||: || :| | ||: | ||:| |:: | ||:| | |
 Db 281 DLETRYNEQKAKD-PKGAEKFKSQMNARFQKTVSSLEEEHKRMRKEIEAVHEERVQAMLN 339

Qy 467 DRRRLALENYITAL--QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAA 524
 ::| | :| || | | || |::||| ||| : |: | |::| |
 Db 340 EKKRDATHDYRQALATHVNKPNKHSVLQSLKAYIRAEKDRMHTLNRYRHLLKADSKEAA 399

Qy 525 QIRSQVMTHLRVIYERMNQSLSLLYNVP-----AVA--EEIQDEVDELLOKEQNYS 573
 : | : || | |:| :|::| : | || :: :||| : |
 Db 400 AYKPTVIHRLRYIDLRLINGTLAMLRDFPDLEKYVRPIAVTYWKDYRDEVSPDISVE---- 455

Qy 574 DDVLANMISEPRISYGN--DALMPSLT----ETKTTVELLPVNGEFSLDDLQPWHSFGAD 627
 | | :| : | | | :| : :|| | :: :|
 Db 456 DSELTPIIHDDEFKNAKLDVKAPTTTAKPVKETDNAKVLPTASDSEEEADEYYEDED 515

Qy 628 SVPANT---ENEVEPVDPARP-----AADRGLTTRPGSGLTNIKT 663
 | : :|: || :| | | | | | | | : :
 Db 516 EQVKKTPDMKKKVKVVDIKPKEIKVTIEEEKKAPKLVETSVQTDDEDDDEDSSSSTSES 575

Qy 664 EE-----ISEVKMDAE-----FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGG 709
 :| | |::| | :|| | | | : :
 Db 576 DEDEDKNIKELRVDIEPIIDEPASFYRHD-----KLIQSPEVERSASSVFQPYVLAS 627

Qy 710 VVIATVIVITLVMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFE 766
 : | | | : : | :|| | | | |::| | | | | | | |
 Db 628 AMFITAICIIAFAITNARRRRAMRGFIEVD-VYTPEERHVGVMQVNGYENPTYSFDD 683

RESULT 13

A32758

beta-amyloid-like protein precursor - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 24-Sep-1998

C;Accession: A32758

R;Rosen, D.R.; Martin-Morris, L.; Luo, L.; White, K.

Proc. Natl. Acad. Sci. U.S.A. 86, 2478-2482, 1989

A;Title: A Drosophila gene encoding a protein resembling the human beta-amyloid protein precursor.

A;Reference number: A32758; MUID:89184650; PMID:2494667

A;Accession: A32758
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-886 <ROS>
A;Cross-references: GB:J04516; NID:g158371; PID:g158372
C;Genetics:
A;Gene: FlyBase:Appl
A;Cross-references: FlyBase:FBgn0000108
C;Keywords: transmembrane protein

Query Match 18.2%; Score 737.5; DB 2; Length 886;
Best Local Similarity 24.7%; Pred. No. 5.2e-32;
Matches 235; Conservative 137; Mismatches 313; Indels 265; Gaps 30;

```
Qy      7 LLLLAAWTARALEVPTDGNAGLLA-----EPQIAMFC--GRLNMHMNV-QNGKWDSDPSG 58
      ||| : | | : | | | | : | | : | | : | |
Db      9 LLLRSLWVVLAI-----GTAQVQAASPRWEPQIAVLCEAGQIYQPQYLSEEGRWVTDLSK 63

Qy     59 T---KTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRG---RKQCKTHPHFV 112
      || : | : | | : | | | | : | | : | | : |
Db     64 KTTGPTCLRDKMDLLDYCKKAYPNRDITNIVESSHYQKIGGWCRQGALNAAKCKGSHRWI 123

Qy    113 IPYRCLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMML 172
      | : || | | | | | | : | | | | : | | : | |
Db    124 KPFRCL-GPFQSDALLVPEGCLFDHIHNASRCWPFVRWNQTGAAACQERGMQMRTFAMLL 182

Qy    173 PCGIDKFRGVEFVCCP-----LAEESDNVD---SA 199
      || | | | | | | | : : | | : | |
Db    183 PCGISVFSGVEFVCCPKHFKTDEIHVKKTDLPVMPAAQINSANDELMNDEDDSDNSNYSK 242

Qy    200 DAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEV-----AEV 237
      || || | | | | : : | | : | |
Db    243 DANEDDL-----DEDDLMDGDEEDDMVADEAATAGGSPNTGSSGDSNSGSLDDINA EY 296

Qy    238 EE-EEADDDDEDEDGDEVEEEAEPEYEEA-TERTTSIATTTTTTTESVEEVVREVCSEQA 295
      : | | | : | : | | | | : : : : : : : : : :
Db    297 DSGEEGDNYEEDGAGSESEAEVEASWDQSGGAKVVSLSKSDSSSPSSAPVAPAPEKAPVKS 356

Qy    296 ETGPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQE 355
      | : : : | | | | | | | : | | : | :
Db    357 ESVTSTPQLS-----ASAAAFVAANSNGNSGT-----GAGAPPSTAQPTSD 396

Qy    356 PLARDPVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEE 415
      | | | | | | | | : : : : | | | | : :
Db    397 P-----YFTHFDPHYEHQSYKVSQKRLEESHREKVTRVMKDWS 435

Qy    416 AERQAKNLPKADKKA-----VIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDR 468
      | : : : | | | | : | | | : | | | : | |
Db    436 LEEKYQDMRLADPKAAQSFQKQRTARFQTSVQALEEEGNAEKHQLAAMHQQRVLAHINQR 495

Qy    469 RRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEH-VRMVDP---KKA 524
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Qy    525 QIRSQVMTHLRVIYERMNQSLSLLYNPAVAEEI-----QDEV----- 562
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 Qy 580 MISE-----PRISYGNDALM-----PSLTETKTTVELLPVNG 611
 Db 676 QVAEQQSQPTQSSTQSQAQQQQQEKSLPGKELGPDAALVTAANPNLETTKS----- 726
 Qy 612 EFSLDDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKM 671
 Db 727 EKDLSDTE----YGEATVSTTKVQTVLPTVDDDAVQRAVEDVAAA-----VAHQEA 773
 Qy 672 DAEFRHDSGYEVHHQKLVF-----FAEDVGSNK---GAIIGLMVGGVVIATVIVITLVML 723
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 Qy 724 KKKQYTSIH-HGVVEVDAAVTP-----EERHLSKMQQNGYENPTYKFFE 766
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RESULT 14

S38344

CDEI-binding protein - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 03-May-1996

C;Accession: S38344

R;Hanes, J.; von der Kammer, H.; Kristjansson, G.I.; Scheit, K.H.

Biochim. Biophys. Acta 1216, 154-156, 1993

A;Title: The complete cDNA coding sequence for the mouse CDEI binding protein.

A;Reference number: S38344; MUID:94032480; PMID:8218408

A;Accession: S38344

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-246 <HAN>

A;Cross-references: EMBL:Z22592

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

Query Match 17.4%; Score 706; DB 2; Length 246;
 Best Local Similarity 51.5%; Pred. No. 5e-31;
 Matches 136; Conservative 35; Mismatches 51; Indels 42; Gaps 7;

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 Qy 57 SGTKTCTIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
 Db 75 TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK 132
 Qy 117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
 Db 133 CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSYGMLLPCGV 192
 Qy 177 DKFRGVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAE 236

OM protein - protein search, using sw model

Run on: August 13, 2004, 09:15:49 ; Search time 144.786 Seconds
(without alignments)
1669.522 Million cell updates/sec

Title: US-09-785-215-2
Perfect score: 4058
Sequence: 1 MLPGLALLLLAAWTARALEV.....KMQQNGYENPTYKFFEQMQN 770

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1292805 seqs, 313927144 residues

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	DB	ID	Description

1	4058	100.0	770	9	US-09-794-927-55	Sequence 55, Appl
2	4058	100.0	770	9	US-09-795-847-55	Sequence 55, Appl
3	4058	100.0	770	9	US-09-794-743-55	Sequence 55, Appl
4	4058	100.0	770	9	US-09-794-748-55	Sequence 55, Appl
5	4058	100.0	770	9	US-09-904-987-2	Sequence 2, Appli
6	4058	100.0	770	9	US-09-794-925-55	Sequence 55, Appl
7	4058	100.0	770	9	US-09-681-442-55	Sequence 55, Appl
8	4058	100.0	770	9	US-09-149-718-6	Sequence 6, Appli
9	4058	100.0	770	9	US-09-785-215-2	Sequence 2, Appli
10	4058	100.0	770	10	US-09-848-616-172	Sequence 172, App
11	4058	100.0	770	10	US-09-869-414-55	Sequence 55, Appl
12	4058	100.0	770	10	US-09-548-366-55	Sequence 55, Appl
13	4058	100.0	770	12	US-10-652-927-55	Sequence 55, Appl
14	4058	100.0	770	12	US-10-652-830-55	Sequence 55, Appl
15	4058	100.0	770	14	US-10-217-584-5	Sequence 5, Appli
16	4058	100.0	770	14	US-10-204-362-2	Sequence 2, Appli
17	4058	100.0	770	14	US-10-169-580-5	Sequence 5, Appli
18	4058	100.0	770	14	US-10-335-035-3	Sequence 3, Appli
19	4058	100.0	770	14	US-10-223-809A-2	Sequence 2, Appli
20	4058	100.0	770	14	US-10-010-942B-38	Sequence 38, Appl
21	4058	100.0	770	14	US-10-357-935-3	Sequence 3, Appli
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23	4058	100.0	770	14	US-10-050-898-218	Sequence 218, App
24	4058	100.0	770	15	US-10-427-208-75	Sequence 75, Appl
25	4058	100.0	770	15	US-10-428-487-12	Sequence 12, Appl
26	4058	100.0	770	16	US-10-388-389-38	Sequence 38, Appl
27	4058	100.0	770	16	US-10-281-092-10	Sequence 10, Appl
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30	4058	100.0	772	9	US-09-795-847-59	Sequence 59, Appl
31	4058	100.0	772	9	US-09-794-743-59	Sequence 59, Appl
32	4058	100.0	772	9	US-09-794-748-59	Sequence 59, Appl
33	4058	100.0	772	9	US-09-794-925-59	Sequence 59, Appl
34	4058	100.0	772	9	US-09-681-442-59	Sequence 59, Appl
35	4058	100.0	772	10	US-09-869-414-59	Sequence 59, Appl
36	4058	100.0	772	10	US-09-548-366-59	Sequence 59, Appl
37	4058	100.0	772	12	US-10-652-927-59	Sequence 59, Appl
38	4058	100.0	772	12	US-10-652-830-59	Sequence 59, Appl
39	3943.5	97.2	751	9	US-09-794-927-57	Sequence 57, Appl
40	3943.5	97.2	751	9	US-09-795-847-57	Sequence 57, Appl
41	3943.5	97.2	751	9	US-09-794-743-57	Sequence 57, Appl
42	3943.5	97.2	751	9	US-09-794-748-57	Sequence 57, Appl
43	3943.5	97.2	751	9	US-09-794-925-57	Sequence 57, Appl
44	3943.5	97.2	751	9	US-09-681-442-57	Sequence 57, Appl
45	3943.5	97.2	751	9	US-09-149-718-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-794-927-55

; Sequence 55, Application US/09794927

; Patent No. US20010016324A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

```

; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-927-55

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Query Match          100.0%; Score 4058; DB 9; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.4e-257;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Qy    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEAETGPC 300
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RESULT 2

US-09-795-847-55

; Sequence 55, Application US/09795847

; Patent No. US20010018208A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
 AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280DE

; CURRENT APPLICATION NUMBER: US/09/795,847

; CURRENT FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-847-55

Query Match 100.0%; Score 4058; DB 9; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.4e-257;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

US-09-794-748-55

; Sequence 55, Application US/09794748

; Patent No. US20020037315A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
 AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280JL

; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-748-55

Query Match 100.0%; Score 4058; DB 9; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.4e-257;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
QY	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
QY	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
QY	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
QY	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVREVCSEQAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVREVCSEQAETGPC	300
QY	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
QY	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
QY	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
QY	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540

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Db      481  ||||| QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
Qy      541  MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600
Db      541  ||||| MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600
Qy      601  KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 660
Db      601  ||||| KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 660
Qy      661  IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
Db      661  ||||| IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
Qy      721  VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
Db      721  ||||| VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

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RESULT 5

US-09-904-987-2

; Sequence 2, Application US/09904987

; Patent No. US20020037908A1

; GENERAL INFORMATION:

; APPLICANT: No. US20020037908A1actyl, Inc.

; TITLE OF INVENTION: Methods and Compositions for Controlling Pathological and Prepathological

; TITLE OF INVENTION: Protein Assembly or Aggregation

; FILE REFERENCE: 42108/26146

; CURRENT APPLICATION NUMBER: US/09/904,987

; CURRENT FILING DATE: 2001-07-12

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 770

; TYPE: PRT

; ORGANISM: homo sapiens

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: NCBI ENTREZ / QRHUA4

; DATABASE ENTRY DATE: 2000-09-15

; RELEVANT RESIDUES: (1)..(770)

US-09-904-987-2

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Query Match          100.0%; Score 4058; DB 9; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.4e-257;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db      1  ||||| MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Qy     61  TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Db     61  ||||| TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Qy    121  EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

```

Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDEGDGDEVEEEAEOPYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDEGDGDEVEEEAEOPYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTET	600
Db	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 6

US-09-794-925-55

; Sequence 55, Application US/09794925

; Patent No. US20020064819A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-925-55

Query Match 100.0%; Score 4058; DB 9; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.4e-257;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480

Qy 481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAQIRSQVMTHLRVIYER 540
 |||
 Db 481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAQIRSQVMTHLRVIYER 540
 |||
 Qy 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600
 |||
 Db 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600
 |||
 Qy 601 KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 660
 |||
 Db 601 KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 660
 |||
 Qy 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 |||
 Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 |||
 Qy 721 VMLKKKQYTSIHGHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
 |||
 Db 721 VMLKKKQYTSIHGHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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RESULT 7

US-09-681-442-55

; Sequence 55, Application US/09681442

; Patent No. US20020081634A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280FG

; CURRENT APPLICATION NUMBER: US/09/681,442

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 55

; LENGTH: 770

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-681-442-55

Query Match 100.0%; Score 4058; DB 9; Length 770;
 Best Local Similarity 100.0%; Pred. No. 2.4e-257;

Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLPG LALLLLA AWTA RALEVP TDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
      |||||||
Db      1 MLPG LALLLLA AWTA RALEVP TDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      |||||||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      |||||||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
      |||||||
Db    181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy    241 EADDDDEDDEDGDEVEEEAEEP YEEATERTTSIATTTTTTTTESVEEVVREVCSEAETGPC 300
      |||||||
Db    241 EADDDDEDDEDGDEVEEEAEEP YEEATERTTSIATTTTTTTTESVEEVVREVCSEAETGPC 300

Qy    301 RAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360
      |||||||
Db    301 RAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360

Qy    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420
      |||||||
Db    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy    421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480
      |||||||
Db    421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy    481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
      |||||||
Db    481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy    541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGN DALMPSLTET 600
      |||||||
Db    541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGN DALMPSLTET 600

Qy    601 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 660
      |||||||
Db    601 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy    661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
      |||||||
Db    661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy    721 VMLKKKQYTSIH HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QN 770
      |||||||
Db    721 VMLKKKQYTSIH HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QN 770
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RESULT 8
US-09-149-718-6

; Sequence 6, Application US/09149718
 ; Patent No. US20020104104A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dora K. Games, Dale B. Schenk, Lisa C. McConlogue,
 ; APPLICANT: Peter A. Seubert, and Russell E. Rydel
 ; TITLE OF INVENTION: Method For Identifying Alzheimer's Disease
 ; TITLE OF INVENTION: Therapeutics Using Transgenic Animal Models
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Patrea L. Pabst
 ; STREET: 2800 One Atlantic Center
 ; STREET: 1201 West Peachtree Street
 ; CITY: Atlanta
 ; STATE: GA
 ; COUNTRY: USA
 ; ZIP: 30309-3450
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/149,718
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/660,487
 ; FILING DATE:
 ; APPLICATION NUMBER: 08/480,653
 ; FILING DATE: June 7, 1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pabst, Patrea L.
 ; REGISTRATION NUMBER: 31,284
 ; REFERENCE/DOCKET NUMBER: ANS101CIP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (404)-873-8794
 ; TELEFAX: (404)-873-8795
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 770 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-149-718-6

Query Match 100.0%; Score 4058; DB 9; Length 770;
 Best Local Similarity 100.0%; Pred. No. 2.4e-257;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDS	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDS	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120

Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN	770
Db	721	VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN	770

RESULT 9

US-09-785-215-2

; Sequence 2, Application US/09785215

; Publication No. US20020187157A1

; GENERAL INFORMATION:

; APPLICANT: JENSEN, Martin Roland et al.

; TITLE OF INVENTION: NOVEL METHOD FOR DOWN-REGULATION OF AMYLOID

; FILE REFERENCE: 3631-0107P

; CURRENT APPLICATION NUMBER: US/09/785,215

; CURRENT FILING DATE: 2001-02-20

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-785-215-2

Query Match 100.0%; Score 4058; DB 9; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.4e-257;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDS	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDS	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVI	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVI	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLL	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLL	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVREVC	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVREVC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKT	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKT	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVM	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVM	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLA	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLA	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVM	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVM	540
Qy	541	MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDA	600
Db	541	MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDA	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTR	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTR	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVI	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVI	720

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Qy      721 VMLKKKQYTSIH HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
          |||||||
Db      721 VMLKKKOYTSIH HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

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RESULT 10
US-09-848-616-172
; Sequence 172, Application US/09848616
; Publication No. US20030054010A1
; GENERAL INFORMATION:
; APPLICANT: Sebbel, Peter
; APPLICANT: Dunant, Nicolas
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0180002
; CURRENT APPLICATION NUMBER: US/09/848,616
; CURRENT FILING DATE: 2001-05-05
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 172
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-848-616-172

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Query Match      100.0%;   Score 4058;   DB 10;   Length 770;
Best Local Similarity 100.0%;   Pred. No. 2.4e-257;
Matches 770;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;
```

[illegible]

Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 11

US-09-869-414-55

; Sequence 55, Application US/09869414

; Publication No. US20030077226A1

; GENERAL INFORMATION:

; APPLICANT: Beinkowski et al.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280M

; CURRENT APPLICATION NUMBER: US/09/869,414

; CURRENT FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 55

; LENGTH: 770

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-869-414-55

Query Match 100.0%; Score 4058; DB 10; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.4e-257;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEEPYYEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEEPYYEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN	770
Db	721	VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN	770

RESULT 12
 US-09-548-366-55
 ; Sequence 55, Application US/09548366
 ; Publication No. US20030104365A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gurney, Mark E.
 ; APPLICANT: Bienkowski, Michael J.
 ; APPLICANT: Heinrikson, Robert L.
 ; APPLICANT: Parodi, Luis A.
 ; APPLICANT: Yan, Riqiang
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
 AND
 ; TITLE OF INVENTION: USES THEREFOR
 ; FILE REFERENCE: 28341/6280A
 ; CURRENT APPLICATION NUMBER: US/09/548,366
 ; CURRENT FILING DATE: 2000-04-12
 ; PRIOR APPLICATION NUMBER: 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 60/101,594
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 65
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 55
 ; LENGTH: 770
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-548-366-55

Query Match 100.0%; Score 4058; DB 10; Length 770;
 Best Local Similarity 100.0%; Pred. No. 2.4e-257;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300

Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNLALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNLALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 13

US-10-652-927-55

; Sequence 55, Application US/10652927

; Publication No. US20040043408A1

; GENERAL INFORMATION:

; APPLICANT: Gurney et al.

; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses

; TITLE OF INVENTION: Therefor

; FILE REFERENCE: 29915/6280N3

; CURRENT APPLICATION NUMBER: US/10/652,927

; CURRENT FILING DATE: 2003-08-29

; PRIOR APPLICATION NUMBER: 09/794,925

; PRIOR FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-652-927-55

Query Match 100.0%; Score 4058; DB 12; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.4e-257;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEI SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720

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|||||
Db      661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
Qy      721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 770
      |||||
Db      721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 770
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RESULT 14

US-10-652-830-55

; Sequence 55, Application US/10652830

; Publication No. US20040048303A1

; GENERAL INFORMATION:

; APPLICANT: Gurney et al.

; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor
and Uses

; TITLE OF INVENTION: Therefor

; FILE REFERENCE: 29915/6280N1

; CURRENT APPLICATION NUMBER: US/10/652,830

; CURRENT FILING DATE: 2003-08-29

; PRIOR APPLICATION NUMBER: 09/794,925

; PRIOR FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 55

; LENGTH: 770

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-652-830-55

Query Match 100.0%; Score 4058; DB 12; Length 770;

Best Local Similarity 100.0%; Pred. No. 2.4e-257;

Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
      |||||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      |||||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      |||||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
```

Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTET	600
Db	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 15

US-10-217-584-5

; Sequence 5, Application US/10217584

; Publication No. US20030077261A1

; GENERAL INFORMATION:

; APPLICANT: Paris, Daniel

; APPLICANT: Mullan, Michael

; TITLE OF INVENTION: Modulation of Angiogenesis by A-Beta Peptides

; FILE REFERENCE: USF-T161XC1

; CURRENT APPLICATION NUMBER: US/10/217,584

; CURRENT FILING DATE: 2002-08-12

; PRIOR APPLICATION NUMBER: 60/311,656

; PRIOR FILING DATE: 2001-08-10

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 770

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(770)
; OTHER INFORMATION: Amyloid precursor protein
US-10-217-584-5
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Query Match          100.0%;  Score 4058;  DB 14;  Length 770;
Best Local Similarity 100.0%;  Pred. No. 2.4e-257;
Matches 770;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
```

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAIVIVITL	720

|||||
Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

|||||
Db 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

Search completed: August 13, 2004, 09:33:23
Job time : 147.786 secs

OM protein - protein search, using sw model

Run on: August 13, 2004, 09:07:53 ; Search time 117.521 Seconds
(without alignments)
2067.275 Million cell updates/sec

Title: US-09-785-215-2
Perfect score: 4058
Sequence: 1 MLPGLALLLLAAWTARALEV.....KMQQNGYENPTYKFFEQMQN 770

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%
Result Query
No. Score Match Length DB ID Description

1	3719.5	91.7	751	13	Q9DGJ7	Q9dgj7 gallus gall
2	3403.5	83.9	747	13	Q91963	Q91963 xenopus. ap
3	3377.5	83.2	695	13	Q9DGJ8	Q9dgj8 gallus gall
4	3163.5	78.0	693	13	Q98SG0	Q98sg0 xenopus lae
5	3152.5	77.7	695	13	Q98SF9	Q98sf9 xenopus lae
6	3150.5	77.6	695	13	Q7ZXQ0	Q7zxq0 xenopus lae
7	2914	71.8	699	13	O57394	O57394 narke japon
8	2785.5	68.6	738	13	Q90W28	Q90w28 brachydanio
9	2717	67.0	569	13	Q9PVL1	Q9pvl1 gallus gall
10	2562.5	63.1	534	13	O93296	O93296 gallus gall
11	2516.5	62.0	678	13	Q7ZZT1	Q7zzt1 brachydanio
12	2437	60.1	694	13	Q8UUR9	Q8uur9 brachydanio
13	2288.5	56.4	612	13	Q9I9E7	Q9i9e7 brachydanio
14	1960.5	48.3	763	11	Q61482	Q61482 mus musculu
15	1956.5	48.2	751	11	Q60709	Q60709 mus musculu
16	1928	47.5	384	11	Q8BPC7	Q8bpc7 mus musculu
17	1733.5	42.7	695	4	Q13861	Q13861 homo sapien
18	1721	42.4	669	4	Q14662	Q14662 homo sapien
19	1713.5	42.2	707	11	Q80US7	Q80us7 mus musculu
20	1709.5	42.1	695	11	Q64348	Q64348 mus musculu
21	1700.5	41.9	715	11	Q7TT34	Q7tt34 mus musculu
22	1604.5	39.5	472	13	Q8UUS0	Q8uus0 brachydanio
23	1350.5	33.3	357	13	Q8UUI8	Q8uui8 brachydanio
24	1302	32.1	523	4	Q14594	Q14594 homo sapien
25	1267	31.2	522	4	Q9BT36	Q9bt36 homo sapien
26	1090	26.9	218	11	Q8BPV5	Q8bpv5 mus musculu
27	795	19.6	357	13	Q7ZZT2	Q7zzt2 brachydanio
28	788	19.4	160	11	Q9QZ78	Q9qz78 cavia sp. p
29	771	19.0	239	13	Q8UUI7	Q8uui7 brachydanio
30	577	14.2	113	13	Q8JH58	Q8jh58 chelydra se
31	561	13.8	182	11	Q9CYS4	Q9cys4 mus musculu
32	478	11.8	97	6	Q28673	Q28673 oryctolagus
33	435.5	10.7	140	13	Q800X9	Q800x9 chelydra se
34	393.5	9.7	82	4	Q16019	Q16019 homo sapien
35	389.5	9.6	82	4	Q16014	Q16014 homo sapien
36	387.5	9.5	82	4	Q16020	Q16020 homo sapien
37	376	9.3	79	11	O35463	O35463 cricetus
38	335	8.3	208	11	Q8R0R7	Q8r0r7 mus musculu
39	282	6.9	82	13	Q7ZZT3	Q7zzt3 brachydanio
40	239	5.9	49	6	O97917	O97917 bos taurus
41	207	5.1	3198	5	Q9U8G8	Q9u8g8 manduca sex
42	205.5	5.1	759	5	Q8IT91	Q8it91 ancylostoma
43	194.5	4.8	2225	5	O45881	O45881 caenorhabdi
44	187	4.6	2772	5	Q9VAV4	Q9vav4 drosophila
45	187	4.6	2776	5	Q869A0	Q869a0 drosophila

ALIGNMENTS

RESULT 1

Q9DGJ7

ID Q9DGJ7 PRELIMINARY; PRT; 751 AA.
AC Q9DGJ7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Beta-amyloid precursor protein 751 isoform.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sarasa M., Rodolosse A., Sorribas V.;
 RT "Cloning of full-length chicken beta-amyloid precursor protein
 RT isoforms."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF289219; AAG00594.1; -.
 DR HSSP; P05067; 1BA4.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match 91.7%; Score 3719.5; DB 13; Length 751;
 Best Local Similarity 91.7%; Pred. No. 6.9e-220;
 Matches 708; Conservative 18; Mismatches 23; Indels 23; Gaps 4;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPHLALLLLAAGAARALEVPADGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGWKQCNGHPHIVVPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKLLHQERMDVCETHLHWHTVAKESCSEKSMNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVE--VAEEEEVAEVE	238
Db	181	GVEFVCCPLAEESDNLDSADAEEDSDVWWGGADADYADGSDDKVVEEQPEEDEELTVVE	240
Qy	239	EEEADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEAETG	298
		: : :	

Db 241 DEDADDD-DDDDGDEI-EETEEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETG 298

Qy 299 PCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLA 358
 |||||:|||||

Db 299 PCRAMISRWFYFDVAEGKCAPFFYGGCGGNRNNFDSEYCMVCGSV----- 344

Qy 359 RDPVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAER 418
 |||||

Db 345 -----LPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAER 399

Qy 419 QAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYIT 478
 |||||:|||||

Db 400 QAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRIALENYIT 459

Qy 479 ALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIY 538
 |||

Db 460 ALQTVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIY 519

Qy 539 ERMNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSLT 598
 |||||

Db 520 ERMNQSLSLFLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSLT 579

Qy 599 ETKTTVELLPVNGEFSDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGL 658
 |||||:|||||

Db 580 ETKTTVELLPVDGEFSDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGL 639

Qy 659 TNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVI 718
 ||:||||:|||||

Db 640 TNVKTEEVSEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVI 699

Qy 719 TLVMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
 |||||

Db 700 TLVMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 751

RESULT 2

Q91963

ID Q91963 PRELIMINARY; PRT; 747 AA.

AC Q91963;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE APP747.

GN APP747.

OS Xenopus.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae.

OX NCBI_TaxID=8353;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93129227; PubMed=1282805;

RA Okado H., Okamoto H.;

RT "A Xenopus homologue of the human beta-amyloid precursor protein:
 developmental regulation of its gene expression.";

RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).

DR EMBL; S52417; AAB24853.1; -.

DR HSSP; P05067; 1HZ3.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 747 AA; 84893 MW; A75E81885681D948 CRC64;

Query Match 83.9%; Score 3403.5; DB 13; Length 747;
 Best Local Similarity 85.2%; Pred. No. 1.7e-200;
 Matches 645; Conservative 40; Mismatches 45; Indels 27; Gaps 5;

Qy	17	ALEVPTDGNAGLLAEPQIAMF-CGRLNMHMNVQNGKWSDPSGKTCTCIDTKEGILQYCQE	75
Db	15	ALEVLVDGNGGLLAEPQIAMFSVARLNMHMNVQNGKWETDVSG---CIGTKEGILQYCQE	71
Qy	76	VYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDALLVPDKCKF	135
Db	72	VYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVGEFVSDALLVPDKCKF	131
Qy	136	LHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVFVCCPLAEESDN	195
		: : : : :	
Db	132	LHQERMDICETHLHWHTVAKESCSEKSM LHEYGMLLPCGIDKFRGVFVCCPSAEES	191
Qy	196	VDSADAEEDDSVWVGADTDYADGSEDKVVEVA--EEEEVAEVEEEEADDDDEDGDE	253
		:	
Db	192	FDSADAEEDDCDVWVGADADYVDRSDDKAVEAQPDEEEVVEVEEEEETDDDED--DGDE	249
Qy	254	VEEEAEPEPYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPCRAMISRWFYDVTE	313
		:	
Db	250	AEEPEPEPYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPCRAMISRWFYDVTE	309
Qy	314	GKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARDPVKLPTTAASTPD	373
		: :	
Db	310	SKCAQFIYGGCGGNRNNFESDDYCMVCGSV-----IPATAASTPD	350
Qy	374	AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQ	433
		: : :	
Db	351	AVDKYLENPNDENEHDFLKAERLEGGHREKMSVMEKEWEAEERQAKNLPKADKKAVIQ	410
Qy	434	HFQEKVESLEQEAAANERQQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFN	493
		:	
Db	411	HFQEKVESLEQEAAKQRQQQLVETHMARVEAMLNDRRRIALENYITALQADPPRPRHVFN	470

Qy	494	LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPA	553
Db	471	LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVPA	530
Qy	554	VAEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEF	613
Db	531	VAEEIQDEVDELQKEQNYSDDMVSNMVSDHRVSYGNDALMPSLSETKTTVELLPVDGEF	590
Qy	614	SLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDA	673
		::	
Db	591	NIEDLQPWHSFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDS	650
Qy	674	EFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHH	733
		::	
Db	651	EYRHDTAYEVHHQKLVFFAEVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTTIHH	710
Qy	734	GVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMQN	770
Db	711	GVVEVDAAVTPEERHLTKMQQNGYENPTYKFFEOMON	747

Q9DGJ8

Query Match 83.2%; Score 3377.5; DB 13; Length 695;
Best Local Similarity 84.7%; Pred. No. 6e-199;
Matches 654; Conservative 18; Mismatches 21; Indels 79; Gaps 4;

83.2%; Score 3377.5; DB 13; Length 695;

Best Local Similarity 84.7%; Pred. No. 6e-199;

Matches 654; Conservative 18; Mismatches 21; Indels 79; Gaps 4;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPHLALLLLAAGAARALEVPADGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGWKQCNGHPHIVVPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKLLHQERMDVCETHLHWHTVAKESCSEKSMNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVE--VAEEEEVAEVE	238
Db	181	GVEFVCCPLAEESDNLDSADAEDDDSDVWWGGADADYADGSDDKVVEEQPEEDEELTVVE	240
Qy	239	EEEADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETG	298
		: : : :	
Db	241	DEDADDD-DDDDGDEI-EETEEYEEATERTTSIATTTTTTTESVEEVVR-----	288
Qy	299	PCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLKTTQEPLA	358
Db	289	-----	288
Qy	359	RDPVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAER	418
		:	
Db	289	-----VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAER	343
Qy	419	QAKNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYIT	478
Db	344	QAKNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRIALENYIT	403
Qy	479	ALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIY	538
Db	404	ALQTVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIY	463
Qy	539	ERMNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLT	598
Db	464	ERMNQSLSFLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLT	523
Qy	599	ETKTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGL	658
Db	524	ETKTTVELLPVDGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGL	583
Qy	659	TNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVI	718
		: :	
Db	584	TNVKTEEVSSEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVI	643
Qy	719	TLVMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	644	TLVMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	695

RESULT 4

Q98SG0

ID Q98SG0

PRELIMINARY;

PRT;

693 AA.

AC Q98SG0;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Beta-amyloid precursor protein A.
 GN APP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Van den Hurk W.H.;
 RL Thesis (2001), Department of Biological Sciences,
 RL University of Nijmegen, Nijmegen, Netherlands.
 DR EMBL; AJ298150; CAC37193.1; -.
 DR HSSP; P05067; 1H23.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 KW Signal.
 FT SIGNAL 1 18 POTENTIAL.
 SQ SEQUENCE 693 AA; 78568 MW; CAF1DF655C1AB653 CRC64;

Query Match 78.0%; Score 3163.5; DB 13; Length 693;
 Best Local Similarity 79.1%; Pred. No. 8e-186;
 Matches 611; Conservative 37; Mismatches 43; Indels 81; Gaps 5;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK 60
 ||| : ||:| | |||| | | ||||| : ||||| : |||
 Db 1 MLPHITLLVLTG-GALALEVPADGNGGLLAEPQIAMFCGKLNMHMNVQNGKWETDVSGTK 59
 Qy 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
 || ||||| : ||||| : ||| : |||||
 Db 60 GCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVG 119
 Qy 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
 ||||| : ||||| : |||| : ||:|||||
 Db 120 EFVSDALLVPDKCKFLHQERMDICETHLHWHTVAKESCSEKSMMLHEYGMLLPCGIDKFR 179
 Qy 181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVA--EEEEVAEVE 238
 ||||| ||||: |||| |||| |||| | | :|| || ||||| |||
 Db 180 GVEFVCCPSAESESEFDSADA-EDDSDAWWGGADADYVDRSDDKAVEAQPDEEEVVEVE 238
 Qy 239 EEEADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEAETG 298
 ||| |||| | ||| || ||||| : ||||| : |||||
 Db 239 EEETDDDED--DGDEAEPEPEPEYEEATERTTSIATTTTTTTESVEEVVR----- 286
 Qy 299 PCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLA 358

Db	287	-----		286
Qy	359	RDPVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAER	418	
		: : : : :		
Db	287	-----VPATAASTPDAVDKYLENPNDENEHDFLKAKERLEGKHREKMSEVMKEWEEAER	341	
Qy	419	QAKNLPKADKKAVIQHFQEKVESLEQEAAENERQQLVETHMARVEAMLNDRRRLALENYIT	478	
		:		
Db	342	QAKNLPKADKKAVIQHFQEKVESLEQEAAENERQQLVETHMARVEAMLNDRRRIALENYIT	401	
Qy	479	ALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAQAIRSQVMTHLRVIY	538	
Db	402	ALQADPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAQAIRSQVMTHLRVIN	461	
Qy	539	ERMNQSLSLLYNPVAVAEEIQDEVDELLOKEQNYSDDVLANMISEPRISYGNDALMPSLT	598	
		: : : : : : : : : :		
Db	462	ERMNQSFSLLYKVPVAVAEEIQDEVDELFQKEQNYSDDMVSNMVSDDRHSYGNDALMPSLS	521	
Qy	599	ETKTTVELLPVNGEFSDDLQPWHSGFADSVPANTENEVEPVDPARPAADRGLTTRPGSGL	658	
		: : : : : : : : : : : : : : : :		
Db	522	ETKTTVELLPVDGEFNIEDLQPWHSGFVDSVPANTENEVEPVDPARPAADRGLTTRPGSGL	581	
Qy	659	TNIKTEEI SEVKMDAEFRHDSGYEVHHQKL VFFAEDVG SNKGAI IGL MVGGV VIATVIVI	718	
		: : : : : : : : : : : : : : : :		
Db	582	TNIKTEEI SEVKMDSEYRHDTAYEVHHQKL VFFAEEVGS NKGAI IGL MVGGV VIATVIVI	641	
Qy	719	TLVMLKKKQYTSIH HGVVEVDAAVTPEERHL SKMQONGYENPTYKF FEQM QN	770	
		: :		
Db	642	TLVMLKKKQYT TIH HGVVEVDAAVTPEERHL TKMQONGYENPTYKF FEOMON	693	

Qy	659	TNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV	IATVIVI	718
Db	584	TNIKREEISEVKMDSEYRHDAAYEVHHQKLVFFADEVGSNKGAIIGLMVGGVV	IATVIVI	643
Qy	719	TLVMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFE	QMQN	770
Db	644	TLVMLKKKQYTTIHGGVVEVDAAVTPEERHLTKMQONGYENPTYKFFE	OMON	695

RESULT 6

Q7ZX00

```

ID      Q7ZXQ0          PRELIMINARY;          PRT;          695 AA.
AC      Q7ZXQ0;
DT      01-JUN-2003 (TrEMBLrel. 24, Created)
DT      01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Hypothetical protein.
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=8355;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RA      Klein S., Strausberg R.;
RL      Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; BC044324; AAH44324.1; -.
DR      GO; GO:0016020; C:membrane; IEA.
DR      InterPro; IPR008155; A4_APP.
DR      InterPro; IPR008154; A4_extra.
DR      InterPro; IPR001255; Beta-APP.
DR      Pfam; PF02177; A4_EXTRA; 1.
DR      Pfam; PF03494; Beta-APP; 1.
DR      PRINTS; PR00203; AMYLOIDA4.
DR      SMART; SM00006; A4_EXTRA; 1.
DR      PROSITE; PS00319; A4_EXTRA; 1.
DR      PROSITE; PS00320; A4_INTRA; 1.
KW      Hypothetical protein.
SQ      SEQUENCE      695 AA;  78803 MW;  C1BD8AACC3356B05 CRC64;

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Query Match 77.6%; Score 3150.5; DB 13; Length 695;
Best Local Similarity 78.9%; Pred. No. 5e-185;
Matches 609; Conservative 38; Mismatches 46; Indels 79; Gaps 5;

```

Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
      ||| : ||:| | | |||| ||| ||||| ||||| : ||||| ||||| : |||
Db      1 MLPHITLLVLTA-GALALEVPADGNGGLLAEPQIAMFCGKLNMHMNVQNGKWETDVSGTK 59

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      || ||||| ||||| ||||| ||||| ||||| ||||| : ||||| : | |: |||||
Db     60 GCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVG 119

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      ||||| ||||| ||||| ||||| : ||||| ||||| : ||| : ||: ||||| |||||
Db    120 EFVSDALLVPDKCKFLHQERMDICETHLHWHTVAKESCSEKIMSLHEYGMLLPCGIDKFR 179

```

Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEV--AEEEEVAVE	238
		::	
Db	180	GVEFVCCPTAEESFDSADA-EDDSVWWGGADADYVDRSDDKAVEAQPEEEEEVEVE	238
Qy	239	EEEADDDDEDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTTESVEEVVREVCSEQAETG	298
		::	
Db	239	EEEADDD-DDDDGDETEEEPEPEYEEATERTTTSIATTTTTTTTESVEEVVRAV-----	289
Qy	299	PCRAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLKTTQEPLA	358
Db	290	-----	289
Qy	359	RDPVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAER	418
Db	290	-----PATAVSTPDAVDKYLENPNDENEHDFLKAKERLEGKHREKMSEVMKEWEEAER	343
Qy	419	QAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYIT	478
Db	344	QAKNLPKADKKAVIQHFQEKVESLEQEAAKERQQLVETHMARVEATLNDRRRIALENYIT	403
Qy	479	ALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIY	538
Db	404	ALQADPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIN	463
Qy	539	ERMNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLT	598
Db	464	ERMNQSFSLLYKVPAAVEEIQDEVDELQKEQNYSDMVSNMVS DHRVSYGN DALMPSLS	523
Qy	599	ETKTTVELLPVNGEFSDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGL	658
Db	524	ETKTTVELLPVDGEFNVEDLQPWHSFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGL	583
Qy	659	TNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVI	718
Db	584	TNIKREEISEVKMDSEYRHDAAYEVHHQKLVFFADEVGSNKGAIIGLMVGGVVIATVIVI	643
Qy	719	TLVMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN	770
Db	644	TLVMLKKKQYTTIHGVEVDAAVTPEERHLTKMQNGYENPTYKFFEQQMN	695

RESULT 7

O57394

ID O57394 PRELIMINARY; PRT; 699 AA.
AC O57394;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE EL amyloid precursor protein 699.
GN EL APP699.
OS Narke japonica (Electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Hypnosqualia; Pristiorajia; Batoidea;
OC Torpediniformes; Narcinoidei; Narkidae; Narke.
OX NCBI_TaxID=62965;
RN [1]

Db 341 EWEEAERQAKNLPKADKKAVIQRFQEMVESLEQEAASERQQQLVETHMARVEAMLNDRRI 400
 Qy 472 ALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVM 531
 ||||: ||| ||||| | ||| ||||| |||||: ||| |||: |||||: |||
 Db 401 ALENYLAALQADPPRPRHVLNALKKYSRAEQKDRQHTLKHFDHVRAVDPEKAAQIKSQVM 460
 Qy 532 THLRVIYERMNQSLSLLYNVPAAVEEQDEVDPELLQKEQNYSDDLANMISEPRISYGND 591
 ||| || ||||| ||||| ||: ||||| |||||: ||: ||: ||| :|: |||||
 Db 461 THLHVIDERMNQSLSLLYKVPSVAEEIQDEVDPELLQRESYMDDMMANSVSDTRISYGND 520
 Qy 592 ALMPSLTETKTTVELLPVNGEFSDDLQPWHSFGADSVANTENEVEPVDARPAADRGLT 651
 ||: |||: |||||: |||| : ||| ||||| | | : ||: ||||| ||||| |||||
 Db 521 ALVPSLSETKTTELLPDDGEFILDQLPPHPFVIESIPANTENEVEPVDARPAPDRGLT 580
 Qy 652 TRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 711
 ||||| |||||: ||: ||: ||: ||||| ||||| : ||||| ||||| |||||
 Db 581 TRPGSGLTGIKTEEIAELKMETEFQQDSGYEVHHQKLVFFPKDVGSNKGAIIGLMVGGVV 640
 Qy 712 IATVIVITLVMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 770
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 641 IATVIVITLVMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 699

RESULT 8

Q90W28

ID Q90W28 PRELIMINARY; PRT; 738 AA.
 AC Q90W28;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Amyloid precursor protein.
 GN APPA OR APP.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Groth C., Lardelli M.;
 RT "Expression analysis of zebrafish app."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF389401; AAK64495.1; -.
 DR ZFIN; ZDB-GENE-000616-13; appa.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.

Db	121	DD-DDDDGDEI-EETEEYEEATERTTSIATTTTTTTSVEEVVR-----	163
Qy	304	ISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLKTTQEPLARDPVK	363
Db	164	-----	163
Qy	364	LPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNL	423
		:	
Db	164	VPTTAASTPDVVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNL	223
Qy	424	PKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAV	483
		:	
Db	224	PKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRIAILENYITALQTV	283
Qy	484	PPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQ	543
Db	284	PPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAVQIRSQVMTHLRVIYERMNQ	343
Qy	544	SLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTLTETKTT	603
		:	
Db	344	SLSFLYNVPAVAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTLTETKTT	403
Qy	604	VELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKT	663
		:	
Db	404	VELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNVKT	463
Qy	664	EEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVML	723
		:	
Db	464	EEVSEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIANVIVITLVML	523
Qy	724	KKKQYTSIHGHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN	770
Db	524	KKKQYTSIHGHGVVEVDAAVTP-ERHLSKMQQNGYENPTYKFFEQQMN	569

RESULT 10

O93296

ID O93296 PRELIMINARY; PRT; 534 AA.
AC O93296;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amyloid protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
RT substrate for caspase-3 in dying motoneurons."
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL; AF042098; AAC25052.1; -.

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DR      HSSP; P05067; 1BA4.
DR      GO; GO:0016020; C:membrane; IEA.
DR      InterPro; IPR008155; A4_APP.
DR      InterPro; IPR008154; A4_extra.
DR      InterPro; IPR001255; Beta-APP.
DR      Pfam; PF02177; A4_EXTRA; 1.
DR      Pfam; PF03494; Beta-APP; 1.
DR      PRINTS; PR00203; AMYLOIDA4.
DR      PROSITE; PS00319; A4_EXTRA; 1.
DR      PROSITE; PS00320; A4_INTRA; 1.
FT      NON_TER      1      1
SQ      SEQUENCE      534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

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Qy 762 YKFFEOMQN 770
| | | | | | | |
Db 526 YKFFEOMQN 534

RESULT 11

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Q7ZZT1
ID   Q7ZZT1          PRELIMINARY;          PRT;    678 AA.
AC   Q7ZZT1;
DT   01-JUN-2003   (TrEMBLrel. 24, Created)
DT   01-JUN-2003   (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003   (TrEMBLrel. 25, Last annotation update)
DE   Amyloid protein a variant 2.
GN   APPA.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Groth C., Lardelli M.;
RT   "Investigation of zebrafish appa expression during embryogenesis.";
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY271746; AAP22958.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE    678 AA;  76755 MW;  94163778444FD0BC CRC64;

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Query Match 62.0%; Score 2516.5; DB 13; Length 678;
Best Local Similarity 64.8%; Pred. No. 3.9e-146;
Matches 498; Conservative 79; Mismatches 94; Indels 97; Gaps 12;

Qy	5	LALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGR_LNMHMNVQNGKWDSDPSG_TKTCID	64
		: : : : : : : : : : : :	
Db	6	LFILLMAVASTLAVEVPSDSGTGLLAEPQIAMFCG_K_LNMHINIQSGKWEPDPSGSKSCIG	65
Qy	65	TKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVS	124
		: : : : :	
Db	66	NKEGILQYCQEVYPELQITNVVEANQPVSIWDWCKKSRKQCRSHMHIVVPYRCLVGEFVS	125
Qy	125	DALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEF	184
		: : : : :	
Db	126	DALLVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEF	185
Qy	185	VCCPLAEESDNVDSADAEEDSDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEEEADD	244
		: : : : : : : : :	
Db	186	VCCP-ADAGKESESAAVEEDSDSVWWGGAEADYTENSMTR--DAAAEPAV--LEDDEDAD	240

Qy	245	DEDDGDG-VEEEAEPEYEEATERTT-SIATTTTTTTESVVEEVVREVCSEQAETGPCRA	302
		: : : : : : :: :	
Db	241	EEDEDGDGDRDEKIEEEEEERTQSTSAALTSTTTTTTESVVEEVR-----	286
Qy	303	MISRWFVDVTEGKCAPPFFYGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTOEPLARDPV	362
Db	287	-----	286
Qy	363	KLPTTAASTPDAVDKYLET PGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKN	422
		: : : :	
Db	287	-VTPSSSPDAVDRYLET PADENEHAHFLKAKESLETKHRERMSQVMREWEEAERQAKS	345
Qy	423	LPKADKKAVIQHFQEKVESLEQEAAENERQQLVETHMARVEAMLNDRRLALENYITALQA	482
		: : : : :	
Db	346	LPRNDKKAVIQHFQEKVEALEQESASERQQLVETHMARVEALLNDRRLALESYLSALQA	405
Qy	483	VPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMN	542
		:	
Db	406	DPPRPRHVFSLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRPQVLTHLRVIEERMN	465
Qy	543	QSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRI SYGNDALMPSLTETKT	602
		: :	
Db	466	QSLGLLYKVPGVADDIQDQV-ELLQREQQEMSAQLANLQSDARVS YGNDALMPDST--A	521
Qy	603	TVELLPVNGEFSLDDLQPWHSFGADSV PANTENEPVDARPAADRGLTTRPGSGLTNIK	662
		: :	
Db	522	GLELLPAEDTQGFGFIHP-ESFN---QPNTHNQVEPVDARPVPDL DLATRPSVSGL---K	573
Qy	663	TEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAI IGLMVGGVVIATVIVITLVM	722
		: : :	
Db	574	PDDIPELRMEAEERHS---EVYHQKLVFFAEDVSSNKGAI IGLMVGGVVIATIIVITLVM	630
Qy	723	LKKKQYTSIH HGVVEVDAAVTPEERHL SKMQONGYENPTYKFFEOMQN	770
		: :	
Db	631	LRKKOYTSIH HGII EVDAAVTPEERHL SKMOONGYENPTYKFFEOMHN	678

08UUR9

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ID      Q8UUR9          PRELIMINARY;          PRT;      694 AA.
AC      Q8UUR9;
DT      01-MAR-2002   (TrEMBLrel. 20, Created)
DT      01-MAR-2002   (TrEMBLrel. 20, Last sequence update)
DT      01-JUN-2003   (TrEMBLrel. 24, Last annotation update)
DE      Putative membrane protein.
GN      APPB.
OS      Brachydanio rerio (Zebrafish) (Danio rerio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Danio.
OX      NCBI_TaxID=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      PubMed=11862463;
RA      Musa A., Lehrach H., Russo V.E.A.;
RT      "Distinct expression patterns of two zebrafish homologues of the human

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RT APP gene during embryonic development.";
 RL Dev. Genes Evol. 211:563-567(2001).
 DR EMBL; AJ315639; CAC85736.1; -.
 DR ZFIN; ZDB-GENE-020220-1; appb.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 SQ SEQUENCE 694 AA; 79228 MW; 2B03382D411162DC CRC64;

Query Match 60.1%; Score 2437; DB 13; Length 694;
 Best Local Similarity 61.2%; Pred. No. 3e-141;
 Matches 476; Conservative 99; Mismatches 97; Indels 106; Gaps 10;

Qy	7	LLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGKTCTCIDTK	66
		: : : : : : : : : : :	
Db	9	LLMLTTLTLAIEVPSDDSVGLLAEPQVAMFCGKLNMHINVQSGKWEPTDPTGTKSCISTK	68
Qy	67	EGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDA	126
		: : : : : : :	
Db	69	EGILKYCQEVYPDLQITNVVEANQPVSIQNWCKMGRQCRSHTHIVVPYRCLVGEFVSDA	128
Qy	127	LLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVC	186
		: : : : : :	
Db	129	LLVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEFVC	188
Qy	187	CPLAEESDNVDSADAEEDSDVWWGGADTDYADGS--EDKVV-----EVAEEEEVAEVEE	239
		: : : : : : : ::: :	
Db	189	CPMEEQKD-LDSEEQEEANSDVWWGGAETEYTDASVLKEQVTAKPDPVTEDEDEDLNNEE	247
Qy	240	EEADDDDEDEDGDEVEEEAE-----PYEEATERTTTIA--TTTTTTTESVEEVVREVCS	292
		::: :: : :: : : : : :	
Db	248	EEVWDNDEDGDGEDDEDEDDDEDIIDEQDTSEQTSNIAMTTTTTTTTTESIEEVVR----	303
Qy	293	EQAETGPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKT	352
Db	304	-----	303
Qy	353	TQEPLARDPVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMRE	412
		: : : :	
Db	304	-----VPTMAPSPADAVDRYLEAPGDMNEHMRQKAKESLEAKHREKMSEVMRE	352
Qy	413	WEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLA	472
		: : : :	
Db	353	WEEAERQAKNLPKADKKTIIQRFQEKVESLEKEAAGERQQLVETHMARVEALLNDRRRQA	412
Qy	473	LENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMT	532
		: ::: : : : : :	
Db	413	LESYLSSLQSDQPRPRQVLNLLKKYIRAEQKDRQHTLKHFEHVREVDPKKASQIRPFVMT	472
Qy	533	HLRVIYERMNQSLSLLYNPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGND	592

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      ||||| ||||| || || || :|||:| |:|:| |::: |: |:| |||||
Db      473 HLRVIEERMNQSLGYLYKVPQVANDIQDQVAVLVQRDQAEVTQQLSSLQSKMRVSYGNDA 532
Qy      593 LMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTT 652
      ||| |:: |:: || : | : | || ||:| ||||| |::| |
Db      533 LMPDLPDSTTPLDNLPEQD-GLGFIHP-ESFN----QANTDNHVEPVDARPIPERGLPT 586
Qy      653 RPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVI 712
      || ||:|:| | ||:|:| :|:| |||:||||| |||||
Db      587 RP-----EIPKVRLDIEERHNAGYDVRDKRLMFLAEDMGSNKGAIIGLMVGGVVI 636
Qy      713 ATVIVITLVMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
      |||||:|||||:|||||:|||||:|||||
Db      637 ATVIVITLVMLRKKQYTSIHGVIEVDAAVTPEERHLAKMQQNGYENPTYKFFEQMQN 694

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RESULT 13

Q9I9E7

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ID      Q9I9E7          PRELIMINARY;          PRT;          612 AA.
AC      Q9I9E7;
DT      01-OCT-2000 (TrEMBLrel. 15, Created)
DT      01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Amyloid protein (Fragment).
GN      APPA.
OS      Brachydanio rerio (Zebrafish) (Danio rerio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Danio.
OX      NCBI_TaxID=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Slavov D.B., Gardiner K.;
RT      "An App cDNA from Zebrafish (Danio rerio).";
RL      Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AF257742; AAF71748.1; -.
DR      HSSP; P05067; 1HZ3.
DR      ZFIN; ZDB-GENE-000616-13; appa.
DR      GO; GO:0016020; C:membrane; IEA.
DR      InterPro; IPR008155; A4_APP.
DR      InterPro; IPR008154; A4_extra.
DR      InterPro; IPR001255; Beta-APP.
DR      Pfam; PF02177; A4_EXTRA; 1.
DR      Pfam; PF03494; Beta-APP; 1.
DR      PRINTS; PR00203; AMYLOIDA4.
DR      PROSITE; PS00319; A4_EXTRA; 1.
DR      PROSITE; PS00320; A4_INTRA; 1.
FT      NON_TER          1          1
SQ      SEQUENCE          612 AA; 69710 MW; 59A9ACBDF9C59EFF CRC64;

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Query Match          56.4%; Score 2288.5; DB 13; Length 612;
Best Local Similarity 64.7%; Pred. No. 3.3e-132;
Matches 459; Conservative 67; Mismatches 80; Indels 103; Gaps 13;

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Qy      68 GILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDAL 127
      |||||:|||||:|||||:|||||:| | |:| |||||
Db      1 GILQYCQEVYPELQITNVVEANQPVSIWDWCKKSRKQCRSHMHIVVPYRCLVGEFVSDAL 60

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Qy	128	LVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVVEFVCC	187
		: : :	
Db	61	LVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVVEFVCC	120
Qy	188	PLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEEEADDDDED	247
		: : : : : : : : : :	
Db	121	P-ADAGKESESAAVEEDDSVWWGGAEADYTENSMTR--DAAAEPAV--LEDDEDADEEE	175
Qy	248	DEDGD-----EVEEEAEOPYEEATERTT-SIATTTTTTTTESVEEVVREVCSEQAETGPCR	301
		: : : : : :	
Db	176	DEDGDGDRDEKIEEEEEEE--EERTQSTSAALTSTTTTTTTESVDEVVR-----	220
Qy	302	AMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVAVCGSAMSQSLKTTQEPLARDP	361
Db	221	-----	220
Qy	362	VKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAK	421
		: : : :	
Db	221	--VPTPSSSPDAVDRYLETPADENEHAHFLKAKESLETKHRERMSQVMREWEEAERQAK	278
Qy	422	NLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQ	481
		: : : : : : : :	
Db	279	SLPRNDKKAVIQHFQEKVEALEQESASERQQLVETHMARVEALLNDRRRLALESYLSALQ	338
Qy	482	AVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERM	541
		: : :	
Db	339	ADPPRPRHVFSLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRPQVLTHLRVIEERM	398
Qy	542	NQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTETK	601
		: : : : : : :	
Db	399	NQSLGLLYKVPGVADDIQDQV-ELLQREQQEMSAQLANLQSDARVSYGNDAIMPST---	454
Qy	602	TTVELLPVNGEFSDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNI	661
		: : :	
Db	455	AGLELLPAEDTQGFQGFHP-ESFN----QPNTHNQVEPVDARPVDPDLDLATRPVSGL---	506
Qy	662	KTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLV	721
		: : : : : : :	
Db	507	KPDDIPELRMEAEERHS---EVYHQKLVFFAEDVSSNKGAIIGLMVGGVVIATIIVITLV	563
Qy	722	MLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
		: : :	
Db	564	MLRKKQYTSIHGGIIEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	612

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6;
 RX MEDLINE=96299736; PubMed=8661100;
 RA Yang Y., Martin L., Cuzin F., Mattei M.G., Rassoulzadegan M.;
 RT "Genomic structure and chromosomal localization of the mouse CDEI-
 RT binding protein CDEBP (APLP2) gene and promoter sequences.";
 RL Genomics 35:24-29(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6;
 RA Luc M., Yang Y.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U37485; AAB38114.1; -.
 DR EMBL; U37468; AAB38114.1; JOINED.
 DR EMBL; U37469; AAB38114.1; JOINED.
 DR EMBL; U37470; AAB38114.1; JOINED.
 DR EMBL; U37471; AAB38114.1; JOINED.
 DR EMBL; U37472; AAB38114.1; JOINED.
 DR EMBL; U37473; AAB38114.1; JOINED.
 DR EMBL; U37474; AAB38114.1; JOINED.
 DR EMBL; U37475; AAB38114.1; JOINED.
 DR EMBL; U37476; AAB38114.1; JOINED.
 DR EMBL; U37477; AAB38114.1; JOINED.
 DR EMBL; U37478; AAB38114.1; JOINED.
 DR EMBL; U37479; AAB38114.1; JOINED.
 DR EMBL; U37480; AAB38114.1; JOINED.
 DR EMBL; U37481; AAB38114.1; JOINED.
 DR EMBL; U37482; AAB38114.1; JOINED.
 DR EMBL; U37483; AAB38114.1; JOINED.
 DR EMBL; U37484; AAB38114.1; JOINED.
 DR HSSP; P05067; 1MWP.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 763 AA; 86716 MW; 2CDC7780180619A6 CRC64;

Query Match 48.3%; Score 1960.5; DB 11; Length 763;
 Best Local Similarity 49.3%; Pred. No. 5.8e-112;
 Matches 400; Conservative 130; Mismatches 171; Indels 111; Gaps 21;

Qy 5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHNMNVQNGKWDS DP 56

		: :	: : : : :	
Db	15	LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMFCGKLMHVNIQTGKWEPDP	74	
Qy	57	SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR	116	
		: : : : : : : : : : : : : :		
Db	75	TGTSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK	132	
Qy	117	CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI	176	
		: : : : : :		
Db	133	CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSYGMLLPCGV	192	
Qy	177	DKFRGVFVCCPLAE--ESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAE---E	231	
		: : : : : : : : : :		
Db	193	DQFHGTEYVCCPQTKTVDSSTMSKEEEEEEE-----DEEDEEEDYDLKSEFPTE	243	
Qy	232	EEVAEVEEEEAD-DEDEDGDEVEEEAE-----EPYEEATERTTSIATTTTTTTES	282	
		: : : : : : : : : : : :		
Db	244	ADLEDFTEAAADEEEDEEEEGEEVVEDRDYYYDPFKGDDYNE--ENPTEPSSEGTISDKE	301	
Qy	283	VEEVVREVCSEQAETGPCRAMISRWFYDVTGKCAPFFYGGCGGNRNNFDTEEYCMVCG	342	
		: : : : : : : : : : :		
Db	302	IVHDVKAVCSQEAMTGPCRAVMRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMVCK	361	
Qy	343	SAMSQSLLKTTQEPLARDPVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKH	402	
		: : : : : : : : : : : :		
Db	362	AMI-----PPTPLPT-----NDVDVYFETSADDNEHARFQKAKEQLEIRH	401	
Qy	403	RERMSQVMREWEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVE	462	
		: : : : : : : : : :		
Db	402	RNRMDRVKKEWEEAELQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVE	461	
Qy	463	AMLNDRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPAK	522	
		: : : : : : : : : : :		
Db	462	AMLNDRRRIALENYLAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEK	521	
Qy	523	AAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMIS	582	
		:		
Db	522	AAQMKSQVMTHLHVIEERNQSLSLLYKVPYVAQEIQEEIDELLQEQR-----ADM--	572	
Qy	583	EPRI SYGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDA	642	
		: : : : :		
Db	573	-----DQFTSSISENPVDVRVSSESE-EIPPFHPLHPF-----PSLSENE----DT	614	
Qy	643	RPAADRGLTTRPGSGLTN-----IKTEE---ISEVKMDAEFRHDSGYEVHHQKLVFFAED	694	
		: : : : : : : :		
Db	615	QPELYHPM--KKGSGMAEQDGGLIGAEKVINSKNKM DENMVIDETLDV--KEMIFNAER	670	
Qy	695	VGS-----NKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGVE	737	
		: : : : :		
Db	671	VGGLEEEPESVGPLREDFSLSSNALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVE	730	
Qy	738	VDAAVTPEERHLSKMQQNGYENPTYKFFEQQMQ	769	
		: : : :		
Db	731	VDPMLTPEERHLNKMQNHYENPTYKYLEQQMQ	762	

Q60709

ID Q60709 PRELIMINARY; PRT; 751 AA.
AC Q60709;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amyloid precursor-like protein 2, isoform 751.
GN APLP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR;
RA Slunt H.H., Von Koch C., Sisodia S.S.;
RT "Mouse Amyloid Precursor-Like Protein 2 (APLP2) mRNA, isoform APLP2-
RT 751, complete cds.";
RL Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE OF 1-229 FROM N.A.
RC STRAIN=ICR;
RX MEDLINE=94132029; PubMed=8300594;
RA Slunt H.H., Thinakaran G., Von Koch C., Lo A.C., Tanzi R.E.,
RA Sisodia S.S.;
RT "Expression of a ubiquitous, cross-reactive homologue of the mouse
RT beta-amyloid precursor protein (APP).";
RL J. Biol. Chem. 269:2637-2644(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR;
RX MEDLINE=94350957; PubMed=8071334;
RA Thinakaran G., Sisodia S.S.;
RT "Amyloid precursor-like protein 2 (APLP2) is modified by the addition
RT of chondroitin sulfate glycosaminoglycan at a single site.";
RL J. Biol. Chem. 269:22099-22104(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR;
RA Thinakaran G.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U15571; AAA50603.1; -..
DR PIR; A49974; A49974.
DR HSSP; P05067; 1MWP.
DR MGD; MGI:88047; Aplp2.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.

DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 751 AA; 85247 MW; D183F6A4AD17BC04 CRC64;

Query Match 48.2%; Score 1956.5; DB 11; Length 751;
Best Local Similarity 49.3%; Pred. No. 1e-111;
Matches 397; Conservative 130; Mismatches 169; Indels 109; Gaps 20;

Qy 5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWSDP 56
| :||| || | : ||| :|||||||:||||:|:| |||: ||
Db 15 LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPPD 74

Qy 57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
:||||:|: ||| :|||||:|||||||:||||| | :||:| :|||: | |||::
Db 75 TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK 132

Qy 117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
||||||| |||| | :| ||||:||| | |||: || | : | : |||||:|
Db 133 CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSYGMLLPCGV 192

Qy 177 DKFRGVEFVCCPLAE--ESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAE---E 231
|:| | |:|||| : :||: | : ||:: | | || : : :| |
Db 193 DQFHGTEYVCCPQTKTVDSSTMSKEEEEEEE-----DEEDEEEDYDLKSEFPTE 243

Qy 232 EEVAEVEEEEEAD-DEDEDGDEVEEEAE-----EPYEEATERTTSIATTTTTTTES 282
:: : | || :|||:|:| || : : : | | | : : | : :
Db 244 ADLEDFTEAAADEEEEEDEEGEEVVEDRDYYYDPFKGDDYNE--ENPTEPSSEGTISDKE 301

Qy 283 VEEVVREVCSEQAETGPCRAMISRWFYDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVAVCG 342
: | : |||:| |||||:| ||||:|:| || | ||||| |||||:|:| |||||
Db 302 IVHDVKAVCSQEAMTGPCRAVMRWFYDLSKGKCVRFIYGGCGGNRNNFESEDYCMVAVCK 361

Qy 343 SAMSQSLLKTTQEPLARDPVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKH 402
: : | ||| : || | || | :||| |||||:| :|
Db 362 AMI-----PPTPLPT-----NDVDVYFETSADDNEHARFQKAKEQLEIRH 401

Qy 403 RERMSQVMREWEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVE 462
| || :| :||||| ||||| ::: :||| | :||:| ||:|:| |||||:| |||
Db 402 RNRMDRVKKEWEAELQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVE 461

Qy 463 AMLNDRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKK 522
|||||||:|||||: |||: |||| : | :||| ||| ||:|:| || |||:|
Db 462 AMLNDRRRIALENYLAALQSDPPRPHRILQALRRYVRAENKDRRLHTIRHYQHVLAVDPEK 521

Qy 523 AAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDLANMIS 582
|||:| ||||| || || ||||| || ||:| ||:|:| |||||:| :|
Db 522 AAQMKSQVMTHLHVIEERRNQSLSLLYKVPYVAQEIQEEIDELLQEQR-----ADM-- 572

Qy 583 EPRISYGNDALMPSLTETKTTVELLPVNGEFLDDLQPWHSFGADSVFANTENEVEPVDA 642
| | :| | : | : | | | : :|||
Db 573 -----DQFTSSISENPVDVRVSSEESE-EIPPFHPLHPF-----PSLSENE----- 612

Qy 643 RPAADRGLTTRPGSGLTNIKTEEI-SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS---- 697
| : : | || : : | | : || | : | : : :| || ||
Db 613 ----GSGMAEQDG-GLIGAEKVINSKNKMMDENMVIDETLDV--KEMIFNAERVGGLEEE 665

Qy 698 -----NKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGWEVDAAVTP 744
: |:|:| | | | | | |:| |:| |:| |:| |:| |:|
Db 666 PESVGPLREDFSLSSNALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTP 725

Qy 745 EERHLSKMQQNGYENPTYKFFEQMQ 769
| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 726 EERHLNKMQNHHGYENPTYKYLEQMQ 750

Search completed: August 13, 2004, 09:15:34
Job time : 121.521 secs

OM protein - protein search, using sw model

Run on: August 13, 2004, 09:07:28 ; Search time 28.2051 Seconds
(without alignments)
1421.515 Million cell updates/sec

Title: US-09-785-215-2
Perfect score: 4058
Sequence: 1 MLPGLALLLLAAWTARALEV.....KMQQNGYENPTYKFFEQMQN 770

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	ID	Description	
1	4058	100.0	770	1	A4_HUMAN	P05067 h amyloid b	
2	4040	99.6	770	1	A4_MACFA	P53601 m amyloid b	
3	3981	98.1	770	1	A4_PIG	P79307 s amyloid b	
4	3952	97.4	770	1	A4_CAVPO	Q60495 c amyloid b	
5	3937	97.0	770	1	A4_RAT	P08592 r amyloid b	
6	3923	96.7	770	1	A4_MOUSE	P12023 m amyloid b	
7	3921.5	96.6	751	1	A4_SAI SC	Q95241 s amyloid b	
8	2763.5	68.1	780	1	A4_TETFL	O73683 tetraodon f	
9	2699	66.5	737	1	A4_FUGRU	O93279 fugu rubrip	
10	1981.5	48.8	763	1	APP2_HUMAN	Q06481 homo sapien	
11	1971.5	48.6	765	1	APP2_RAT	P15943 rattus norv	
12	1704.5	42.0	695	1	APP2_MOUSE	Q06335 mus musculu	
13	1159.5	28.6	650	1	APP1_HUMAN	P51693 homo sapien	
14	1150.5	28.4	653	1	APP1_MOUSE	Q03157 mus musculu	
15	785	19.3	686	1	A4_CAEEL	Q10651 caenorhabdi	
16	739	18.2	887	1	A4_DROME	P14599 drosophila	
17	403	9.9	76	1	A4_MACMU	P29216 macaca mula	

18	292	7.2	59	1	A4_BOVIN	Q28053	bos taurus
19	288	7.1	58	1	A4_RABIT	Q28748	oryctolagus
20	288	7.1	58	1	A4_SHEEP	Q28757	ovis aries
21	287	7.1	58	1	A4_CANFA	Q28280	canis famil
22	283	7.0	57	1	A4_URSMA	Q29149	ursus marit
23	194.5	4.8	3911	1	AKA9_HUMAN	Q99996	h a-kinase
24	186	4.6	252	1	SPT2_HUMAN	O43291	homo sapien
25	186	4.6	993	1	SCP1_MOUSE	Q62209	mus musculu
26	176	4.3	55	1	ISH1_STOHE	P31713	stoichactis
27	175	4.3	302	1	TFPI_RAT	Q02445	rattus norv
28	174.5	4.3	252	1	SPT2_MOUSE	Q9wu03	mus musculu
29	174.5	4.3	513	1	SPT1_HUMAN	O43278	homo sapien
30	173.5	4.3	1498	1	GOA3_HUMAN	Q08378	homo sapien
31	169	4.2	1875	1	MLP1_YEAST	Q02455	saccharomyc
32	168	4.1	304	1	TFPI_HUMAN	P10646	homo sapien
33	166	4.1	55	1	ISH2_STOHE	P81129	stoichactis
34	164.5	4.1	507	1	SPT1_MOUSE	Q9r097	mus musculu
35	163.5	4.0	346	1	AMBP_MERUN	Q62577	meriones un
36	163.5	4.0	1130	1	YL17_CAEEL	Q11102	caenorhabdi
37	163.5	4.0	2130	1	BA2B_CHICK	Q9de13	gallus gall
38	163	4.0	2944	1	CA17_HUMAN	Q02388	homo sapien
39	163	4.0	3176	1	CA36_HUMAN	P12111	homo sapien
40	162.5	4.0	297	1	TRT2_HUMAN	P45379	homo sapien
41	162	4.0	304	1	TFPI_MACMU	Q28864	macaca mula
42	162	4.0	407	1	IE68_HSVSA	Q01042	herpesvirus
43	162	4.0	3137	1	CA36_CHICK	P15989	gallus gall
44	161.5	4.0	630	1	YCF2_OENVI	P31569	oenothera v
45	161.5	4.0	1278	1	DYNA_HUMAN	Q14203	homo sapien

ALIGNMENTS

RESULT 1

A4_HUMAN

ID A4_HUMAN STANDARD; PRT; 770 AA.
AC P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;
AC Q16019; Q16020; Q9BT38; Q9UCA9; Q9UCB6; Q9UCC8; Q9UCD1; Q9UQ58;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
DE nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP-
DE alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
DE (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
DE (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
DE secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
DE (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
DE (Amyloid intracellular domain 50) (AID(50)); C31].
GN APP OR A4 OR AD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87144572; PubMed=2881207;
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
 RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
 RT cell-surface receptor.";
 RL Nature 325:733-736(1987).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=88122639; PubMed=2893289;
 RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
 RA Cordell B.;
 RT "A new A4 amyloid mRNA contains a domain homologous to serine
 RT proteinase inhibitors.";
 RL Nature 331:525-527(1988).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RX MEDLINE=89128427; PubMed=2783775;
 RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
 RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
 RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
 RT is encoded by 16 exons.";
 RL Nucleic Acids Res. 17:517-522(1989).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM APP770).
 RX MEDLINE=90236318; PubMed=2110105;
 RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene.";
 RL Gene 87:257-263(1990).
 RN [5]
 RP ERRATUM, AND REVISIONS.
 RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
 RL Gene 102:291-292(1991).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
 RC TISSUE=Leukocyte;
 RX MEDLINE=92268136; PubMed=1587857;
 RA Koenig G., Moenning U., Czech C., Prior R., Banati R.,
 RA Schreiter-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
 RT "Identification and differential expression of a novel alternative
 RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
 RT leukocytes and brain microglial cells.";
 RL J. Biol. Chem. 267:10804-10809(1992).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM APP770).
 RX MEDLINE=97263807; PubMed=9108164;
 RA Hattori M., Tsukahara F., Furuhashi Y., Tanahashi H., Hirose M.,
 RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus.";
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM APP639).

RC TISSUE=Brain;
 RX MEDLINE=22744650; PubMed=12859342;
 RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;
 RT "Identification of a novel alternative splicing isoform of human
 RT amyloid precursor protein gene, APP639.";
 RL Eur. J. Neurosci. 18:102-108(2003).
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORM APP305).
 RC TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [10]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [11]
 RP ERRATUM, AND REVISIONS.
 RA Mita S., Sadlock J., Herbert J., Schon E.A.;
 RL Nucleic Acids Res. 16:11402-11402(1988).
 RN [12]
 RP SEQUENCE OF 1-75 FROM N.A.
 RX MEDLINE=89165870; PubMed=2538123;
 RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
 RT "Characterization of the 5'-end region and the first two exons of the
 RT beta-protein precursor gene.";
 RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
 RN [13]
 RP SEQUENCE OF 18-50.
 RC TISSUE=Fibroblast;
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [14]

RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=89346754; PubMed=2569763;
 RA de Sauvage F., Octave J.N.;
 RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
 RT secreted protein.";
 RL Science 245:651-653(1989).
 RN [15]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN [16]
 RP SEQUENCE OF 286-366 FROM N.A.
 RX MEDLINE=88122640; PubMed=2893290;
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530(1988).
 RN [17]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=88122641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity.";
 RL Nature 331:530-532(1988).
 RN [18]
 RP SEQUENCE OF 507-770 FROM N.A.
 RC TISSUE=Brain cortex;
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [19]
 RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
 RX MEDLINE=96139497; PubMed=8576160;
 RA Beher D., Hesse L., Masters C.L., Multhaup G.;
 RT "Regulation of amyloid protein precursor (APP) binding to collagen and
 RT mapping of the binding sites on APP and collagen type I.";
 RL J. Biol. Chem. 271:1613-1620(1996).
 RN [20]
 RP SEQUENCE OF 655-737 FROM N.A., AND VARIANTS AD PHE-717; AD ILE-717
 RP AND AD GLY-717.
 RX MEDLINE=93236601; PubMed=8476439;
 RA Denman R.B., Rosenzwaig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 RT mutations on the processing of the beta-amyloid peptide precursor.";
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
 RN [21]
 RP SEQUENCE OF 656-737 FROM N.A.


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      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA TVIVITL 720

Qy      721 VMLKKKQYTSIH HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 VMLKKKQYTSIH HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

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RESULT 2

A4_MACFA

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ID      A4_MACFA          STANDARD;          PRT;          770 AA.
AC      P53601; Q95KN7;
DT      01-OCT-1996 (Rel. 34, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE      amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE      Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE      APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE      Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE      (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE      secretase C-terminal fragment 50); C31].
GN      APP.
OS      Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC      Cercopithecinae; Macaca.
OX      NCBI_TaxID=9541;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
RC      TISSUE=Cerebellum;
RX      MEDLINE=91273117; PubMed=1905108;
RA      Podlisny M.B., Tolan D.R., Selkoe D.J.;
RT      "Homology of the amyloid beta protein precursor in monkey and human
RT      supports a primate model for beta amyloidosis in Alzheimer's
RT      disease.";
RL      Am. J. Pathol. 138:1423-1435(1991).
CC      -!- FUNCTION: Functions as a cell surface receptor and performs
CC      physiological functions on the surface of neurons relevant to
CC      neurite growth, neuronal adhesion and axonogenesis. Involved in
CC      cell mobility and transcription regulation through protein-protein
CC      interactions (By similarity). Can promote transcription activation
CC      through binding to APBB1/Tip60 and inhibit Notch signaling through
CC      interaction with Numb (By similarity). Couples to apoptosis-
CC      inducing pathways such as those mediated by G(0) and JIP (By
CC      similarity). Inhibits G(0) alpha ATPase activity (By similarity).
CC      Acts as a kinesin I membrane receptor, mediating the axonal
CC      transport of beta-secretase and presenilin 1 (By similarity). May
CC      be involved in copper homeostasis/oxidative stress through copper
CC      ion reduction. In vitro, copper-metallated APP induces neuronal
CC      death directly or is potentiated through Cu(II)-mediated low-
CC      density lipoprotein oxidation (By similarity). Can regulate
CC      neurite outgrowth through binding to components of the
CC      extracellular matrix such as heparin and collagen I and IV (By
CC      similarity). The splice isoforms that contain the BPTI domain
CC      possess protease inhibitor activity (By similarity).
CC      -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators

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CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
 CC (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized to endosomes and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
 CC and nuclei of neurons (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=APP770;
 CC IsoId=P53601-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
 CC -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -!- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 CC similarity).

CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -!- PTM: N- and O-glycosylated (By similarity).
 CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -!- SIMILARITY: Belongs to the APP family.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
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 CC -----
 DR EMBL; M58727; AAA36829.1; -.
 DR EMBL; M58726; AAA36828.1; -.
 DR HSSP; P05067; 1AAP.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KW Proteoglycan; Alternative splicing; Amyloid.
 FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
 FT CHAIN 18 687 SOLUBLE APP-ALPHA (POTENTIAL).
 FT CHAIN 18 671 SOLUBLE APP-BETA (POTENTIAL).
 FT CHAIN 672 770 C99 (POTENTIAL).
 FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (POTENTIAL).
 FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (POTENTIAL).
 FT CHAIN 688 770 C83 (POTENTIAL).
 FT CHAIN 688 713 P3(42) (POTENTIAL).

FT	CHAIN	688	711	P3(40) (POTENTIAL).
FT	CHAIN	712	770	GAMMA-CTF(59) (POTENTIAL).
FT	CHAIN	714	770	GAMMA-CTF(57) (POTENTIAL).
FT	CHAIN	721	770	GAMMA-CTF(50) (POTENTIAL).
FT	CHAIN	740	770	C31 (POTENTIAL).
FT	DOMAIN	18	699	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	700	723	POTENTIAL.
FT	DOMAIN	724	770	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	96	110	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	181	188	ZINC-BINDING (BY SIMILARITY).
FT	DOMAIN	291	341	BPTI/KUNITZ INHIBITOR.
FT	DOMAIN	391	423	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	491	522	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	523	540	COLLAGEN-BINDING (BY SIMILARITY).
FT	DOMAIN	732	751	INTERACTION WITH G(O)-ALPHA
FT				(BY SIMILARITY).
FT	DOMAIN	230	260	ASP/GLU-RICH (ACIDIC).
FT	DOMAIN	274	280	POLY-THR.
FT	SITE	144	144	REQUIRED FOR COPPER(II) REDUCTION
FT				(BY SIMILARITY).
FT	ACT_SITE	301	302	REACTIVE BOND (BY SIMILARITY).
FT	SITE	671	672	CLEAVAGE (BY BETA-SECRETASE)
FT				(BY SIMILARITY).
FT	SITE	672	673	CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT	SITE	687	688	CLEAVAGE (BY ALPHA-SECRETASE)
FT				(BY SIMILARITY).
FT	SITE	704	704	IMPLICATED IN FREE RADICAL PROPAGATION
FT				(BY SIMILARITY).
FT	SITE	706	706	INVOLVED IN OXIDATIVE REACTIONS
FT				(BY SIMILARITY).
FT	SITE	711	712	CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT				(BY SIMILARITY).
FT	SITE	713	714	CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT				(BY SIMILARITY).
FT	SITE	720	721	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT				(BY SIMILARITY).
FT	SITE	724	734	BASOLATERAL SORTING SIGNAL
FT				(BY SIMILARITY).
FT	SITE	739	740	CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)

Query Match 99.6%; Score 4040; DB 1; Length 770;
 Best Local Similarity 99.5%; Pred. No. 6.5e-195;
 Matches 766; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240

Db	181		GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241		EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241		EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301		RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301		RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSVMSQSLRKTREPLTRD	360
Qy	361		PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Db	361		PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Qy	421		KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421		KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481		QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481		QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541		MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Db	541		MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Qy	601		KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601		KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661		IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661		IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721		VMLKKKQYTSIIHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721		VMLKKKQYTSIIHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 3

A4_PIG

ID A4_PIG STANDARD; PRT; 770 AA.

AC P79307; Q29023; Q9TUI0;

DT 01-NOV-1997 (Rel. 35, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kimura A., Takahashi T.;
 RT "Amyloid precursor protein 770.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE OF 1-136 FROM N.A.
 RC TISSUE=Small intestine;
 RA Winteroe A.K., Fredholm M.;
 RT "Evaluation and characterization of a porcine small intestine cDNA
 RT library.";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE OF 667-723 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction (By similarity). In vitro, copper-metallated APP
 CC induces neuronal death directly or is potentiated through Cu(II)-
 CC mediated low-density lipoprotein oxidation (By similarity). Can
 CC regulate neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
 CC (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated

pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CTF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).

-!- DOMAIN: The basolateral sorting signal (BaSS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).

-!- DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).

-!- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields P3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By similarity).

-!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

-!- PTM: N- and O-glycosylated (By similarity).

-!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).

-!- PTM: Extracellular binding and reduction of copper, results in a corresponding oxidation of Cys-144 and Cys-158, and the formation of a disulfide bond (By similarity).

-!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity). Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

-!- SIMILARITY: Belongs to the APP family.

-!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; AB032550; BAA84580.1; -.
 DR EMBL; Z84022; CAB06313.1; -.
 DR EMBL; X56127; CAA39592.1; -.
 DR HSSP; P05067; 1AAP.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KW Amyloid.

FT	SIGNAL	1	17	BY SIMILARITY.
FT	CHAIN	18	770	AMYLOID BETA A4 PROTEIN.
FT	CHAIN	18	687	SOLUBLE APP-ALPHA (POTENTIAL).
FT	CHAIN	18	671	SOLUBLE APP-BETA (POTENTIAL).
FT	CHAIN	672	770	C99 (BY SIMILARITY).
FT	CHAIN	672	713	BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT	CHAIN	672	711	BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT	CHAIN	688	770	C83 (BY SIMILARITY).
FT	CHAIN	688	713	P3(42) (BY SIMILARITY).
FT	CHAIN	688	711	P3(40) (BY SIMILARITY).
FT	CHAIN	712	770	GAMMA-CTF(59).
FT	CHAIN	714	770	GAMMA-CTF(57).
FT	CHAIN	721	770	GAMMA-CTF(50) (BY SIMILARITY).
FT	CHAIN	740	770	C31 (DURING APOPTOSIS) (BY SIMILARITY).
FT	DOMAIN	18	699	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	700	723	POTENTIAL.
FT	DOMAIN	724	770	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	96	110	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	135	155	COPPER-BINDING (BY SIMILARITY).
FT	DOMAIN	181	188	ZINC-BINDING (BY SIMILARITY).
FT	DOMAIN	291	341	BPTI/KUNITZ INHIBITOR.
FT	DOMAIN	391	423	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	491	522	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	523	540	COLLAGEN-BINDING (BY SIMILARITY).
FT	DOMAIN	732	751	INTERACTION WITH G(O)-ALPHA (BY SIMILARITY).
FT	DOMAIN	230	260	ASP/GLU-RICH (ACIDIC).
FT	DOMAIN	274	280	POLY-THR.
FT	SITE	144	144	REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
FT	ACT_SITE	301	302	REACTIVE BOND (BY SIMILARITY).

FT	SITE	671	672	CLEAVAGE (BY BETA-SECRETASE)
FT				(BY SIMILARITY).
FT	SITE	672	673	CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT	SITE	687	688	CLEAVAGE (BY ALPHA-SECRETASE)
FT				(BY SIMILARITY).
FT	SITE	704	704	IMPLICATED IN FREE RADICAL PROPAGATION
FT				(BY SIMILARITY).
FT	SITE	706	706	INVOLVED IN OXIDATIVE REACTIONS
FT				(BY SIMILARITY).
FT	SITE	711	712	CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT				(BY SIMILARITY).
FT	SITE	713	714	CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT				(BY SIMILARITY).
FT	SITE	720	721	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)

Query Match 98.1%; Score 3981; DB 1; Length 770;
 Best Local Similarity 97.8%; Pred. No. 5.8e-192;
 Matches 753; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
		: : : :	
Db	1	MLPGLALVLLAAWTARALEVPTDGNAGLLAEPQVAMFCGKLNMHMNVQNGKWESDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
		: : : :	
Db	61	TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRSRKQCKTHTHIVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
		: : : :	
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
		: : : :	
Db	181	GVEFVCCPLAEESDNIDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVADVVEEEE	240
Qy	241	EADDDDEDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
		: : : : :	
Db	241	EAEDDEDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
		: : : :	
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSVMSQSLLKTTQEHLPOD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAERQA	420
		: : : :	
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
		: : : :	
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
		: : : :	
Db	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
		: : : :	

Db 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDAIMPSLTET 600

Qy 601 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 660
 |||

Db 601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 |||

Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy 721 VMLKKKQYTSIH HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QN 770
 |||

Db 721 VMLKKKQYTSIH HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QN 770

RESULT 4

A4_CAVPO

ID A4_CAVPO STANDARD; PRT; 770 AA.

AC Q60495; Q60496;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
 DE protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
 DE P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57); C31].

GN APP.

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.

OX NCBI_TaxID=10141;

RN [1]

RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.

RC TISSUE=Brain, and Liver;

RX MEDLINE=97236426; PubMed=9116031;

RA Beck M., Mueller D., Bigl V.;

RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
 RT alternative splicing.";

RL Biochim. Biophys. Acta 1351:17-21(1997).

RN [2]

RP INTERACTION OF BETA-APP40 WITH APOE.

RX MEDLINE=98007700; PubMed=9349544;

RA Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,
 RA Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;

RT "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
 RT cerebral capillary sequestration and blood-brain barrier transport of
 RT circulating Alzheimer's amyloid beta.";

RL J. Neurochem. 69:1995-2004(1997).

RN [3]

RP PROCESSING.

RX MEDLINE=20084499; PubMed=10619481;

RA Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
 RA Bigl V.;

RT "Guinea-pig primary cell cultures provide a model to study expression
 RT and amyloidogenic processing of endogenous amyloid precursor

RT protein.";

RL Neuroscience 95:243-254(2000).

RN [4]

RP GAMMA-SECRETASE PROCESSING.

RX MEDLINE=20576391; PubMed=11035007;

RA Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,

RA Ziani-Cherif C., Onstead L., Sambamurti K.;

RT "A novel gamma -secretase assay based on detection of the putative

RT C-terminal fragment-gamma of amyloid beta protein precursor.";

RL J. Biol. Chem. 276:481-487(2001).

CC -!- FUNCTION: Functions as a cell surface receptor and performs

CC physiological functions on the surface of neurons relevant to

CC neurite growth, neuronal adhesion and axonogenesis. Involved in

CC cell mobility and transcription regulation through protein-protein

CC interactions (By similarity). Can promote transcription activation

CC through binding to APBB1/Tip60 and inhibit Notch signaling through

CC interaction with Numb (By similarity). Couples to apoptosis-

CC inducing pathways such as those mediated by G(0) and JIP (By

CC similarity). Inhibits G(0) alpha ATPase activity (By similarity).

CC Acts as a kinesin I membrane receptor, mediating the axonal

CC transport of beta-secretase and presenilin 1 (By similarity). May

CC be involved in copper homeostasis/oxidative stress through copper

CC ion reduction (By similarity). In vitro, copper-metallated APP

CC induces neuronal death directly or is potentiated through Cu(II)-

CC mediated low-density lipoprotein oxidation (By similarity). Can

CC regulate neurite outgrowth through binding to components of the

CC extracellular matrix such as heparin and collagen I and IV (By

CC similarity). The splice isoforms that contain the BPTI domain

CC possess protease inhibitor activity (By similarity).

CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators

CC with metal-reducing activity. Bind transient metals such as

CC copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins

CC and apolipoproteins E and J in the CSF and to HDL particles in

CC plasma, inhibiting metal-catalyzed oxidation of lipoproteins.

CC -!- FUNCTION: Appicans elicit adhesion of neural cells to the

CC extracellular matrix and may regulate neurite outgrowth in the

CC brain (By similarity).

CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved

CC peptides, including C31, are potent enhancers of neuronal

CC apoptosis (By similarity).

CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several

CC cytoplasmic proteins, including APBB family members, the APBA

CC family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also

CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2

CC (via its TPR domains), APPBP2 (via BaSS) and DDB1 (By similarity).

CC Associates with microtubules in the presence of ATP and in a

CC kinesin-dependent manner (By similarity). Soluble Abeta40 binds

CC all three isoforms of APOE, in vitro and in vivo. When lipidated,

CC ApoE3 appears to be the preferred amyloid binding isoform, while

CC the apoE4 isoform-beta-APP40 complex is capable of being

CC transported across the blood-brain barrier.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface

CC protein that rapidly becomes internalized via clathrin-coated pits

CC (By similarity). During maturation, the immature APP (N-

CC glycosylated in the endoplasmic reticulum) moves to the Golgi

CC complex where complete maturation occurs (O-glycosylated and

CC sulfated) (By similarity). After alpha-secretase cleavage, soluble

CC APP is released into the extracellular space and the C-terminal is
 CC internalized to endosomes and lysosomes (By similarity). Some APP
 CC accumulates in secretory transport vesicles leaving the late Golgi
 CC compartment and returns to the cell surface (By similarity). APP
 CC sorts to the basolateral surface in epithelial cells (By
 CC similatity).

CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms, missing exons 7,8 and 15, seem to
 CC exist. The L-isoforms, missing exon 15, are referred to as
 CC appicans;
 CC Name=APP770;
 CC IsoId=Q60495-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;

CC -!- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
 CC brain. The longer isoforms containing the BPTI domain are
 CC predominantly expressed in peripheral organs such as muscle and
 CC liver.

CC -!- INDUCTION: Increased levels during neuronal differentiation.

CC -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells.

CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue (By similarity). The NPXY site is also involved in
 CC clathrin-mediated endocytosis.

CC -!- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
 CC gamma-secretase yields P3 peptides. This is the major secretory
 CC pathway and is nonamyloidogenic. Alternatively,
 CC presenilin/nicastrin-mediated gamma-secretase processing of CTF-
 CC beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
 CC and amyloid-beta 42 (Abeta42), major components of amyloid
 CC plaques, and the corresponding cytotoxic C-terminal fragments
 CC (CTFs).

CC -!- PTM: Proteolytically cleaved by caspase-3 during neuronal
 CC apoptosis (By similarity).

CC -!- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to
 CC the L-APP isoforms produces the APP proteoglycan core proteins,
 CC the appicans (By similarity).

CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific (By similarity).
 CC Phosphorylation can affect APP processing, neuronal
 CC differentiation and interaction with other proteins.

CC -!- PTM: Extracellular binding and reduction of copper, results in a
 CC corresponding oxidation of Cys-144 and Cys-158, and the formation
 CC of a disulfide bond (By similarity).

CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates.
 CC -!- SIMILARITY: Belongs to the APP family.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X97631; CAA66230.1; -.
 DR EMBL; X99198; CAA67589.1; -.
 DR HSSP; P05067; 1BA4.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KW Proteoglycan; Alternative splicing; Amyloid.
 FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
 FT CHAIN 18 687 SOLUBLE APP-ALPHA (BY SIMILARITY).
 FT CHAIN 18 671 SOLUBLE APP-BETA (BY SIMILARITY).
 FT CHAIN 672 770 CTF-ALPHA (BY SIMILARITY).
 FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
 FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
 FT CHAIN 688 770 CTF-BETA (BY SIMILARITY).
 FT CHAIN 688 713 P3(42) (BY SIMILARITY).
 FT CHAIN 688 711 P3(40) (BY SIMILARITY).
 FT CHAIN 712 770 GAMMA-CTF(59) (BY SIMILARITY).
 FT CHAIN 714 770 GAMMA-CTF(57) (BY SIMILARITY).

Query Match 97.4%; Score 3952; DB 1; Length 770;
 Best Local Similarity 96.9%; Pred. No. 1.6e-190;
 Matches 746; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDS DPSG TK 60
 ||| ||||| |||||||||:|||||||: |||||
 Db 1 MLPSLALLLLTTWTARALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWE PDPSG TK 60
 Qy 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
 ||| :||||||| ||||||||| ||||||||| |||||||||

Db	61	TCIGSKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRSRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
		:	
Db	181	GVEFVCCPLAEESDNIDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVADVVEE	240
Qy	241	EADDDDEDDEGDVEVEEEAEEPVEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
		:	
Db	241	EADDDDEDVEDGDVEVEEEAEEPVEEATEKTTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARD	360
		: : :	
Db	301	RSMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVMSQNLLKTSGEPPVSQG	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN	770
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN	770

RESULT 5

A4_RAT

ID A4_RAT STANDARD; PRT; 770 AA.

AC P08592;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
 DE protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains: Soluble
 DE APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-

DE amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);
 DE C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal
 DE fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57);
 DE Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].
 GN APP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=88312583; PubMed=2900758;
 RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
 RA Seeburg P.H.;
 RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
 RT in rat brain suggests a role in cell contact.";
 RL EMBO J. 7:1365-1370(1988).
 RN [2]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89183625; PubMed=2648331;
 RA Kang J., Mueller-Hill B.;
 RT "The sequence of the two extra exons in rat preA4.";
 RL Nucleic Acids Res. 17:2130-2130(1989).
 RN [3]
 RP SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
 RX MEDLINE=21443797; PubMed=11483588;
 RA Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;
 RT "Distinct intramembrane cleavage of the beta-amyloid precursor protein
 RT family resembling gamma-secretase-like cleavage of Notch.";
 RL J. Biol. Chem. 276:35235-35238(2001).
 RN [4]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=96187032; PubMed=8624099;
 RA Sandbrink R., Masters C.L., Beyreuther K.;
 RT "APP gene family. Alternative splicing generates functionally related
 RT isoforms.";
 RL Ann. N.Y. Acad. Sci. 777:281-287(1996).
 RN [5]
 RP TISSUE SPECIFICITY OF APPICAN.
 RX MEDLINE=95263526; PubMed=7744833;
 RA Shioi J., Pangalos M.N., Ripellino J.A., Vassilacopoulou D.,
 RA Mytilineou C., Margolis R.U., Robakis N.K.;
 RT "The Alzheimer amyloid precursor proteoglycan (appican) is present in
 RT brain and is produced by astrocytes but not by neurons in primary
 RT neural cultures.";
 RL J. Biol. Chem. 270:11839-11844(1995).
 RN [6]
 RP TISSUE SPECIFICITY OF ISOFORMS.
 RX MEDLINE=97150061; PubMed=8996834;
 RA Sandbrink R., Monning U., Masters C.L., Beyreuther K.;
 RT "Expression of the APP gene family in brain cells, brain development
 RT and aging.";
 RL Gerontology 43:119-131(1997).
 RN [7]
 RP INTERACTION WITH DDB1, AND MUTAGENESIS OF TYR-757; ASN-759 AND

RP TYR-762.
 RX MEDLINE=99127916; PubMed=9930726;
 RA Watanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,
 RA Suzuki T., Nairn A.C., Greengard P.;
 RT "A 127-kDa protein (UV-DDB) binds to the cytoplasmic domain of the
 RT Alzheimer's amyloid precursor protein.";
 RL J. Neurochem. 72:549-556(1999).
 RN [8]
 RP INTERACTION WITH GNAO1, AND MUTAGENESIS OF 732-HIS-HIS-733.
 RX MEDLINE=99162676; PubMed=10024358;
 RA Brouillet E., Trembleau A., Galanaud D., Volovitch M., Bouilliot C.,
 RA Valenza C., Prochiantz A., Allinquant B.;
 RT "The amyloid precursor protein interacts with Go heterotrimeric
 RT protein within a cell compartment specialized in signal
 RT transduction.";
 RL J. Neurosci. 19:1717-1727(1999).
 RN [9]
 RP CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
 RX MEDLINE=95256193; PubMed=7737970;
 RA Pangalos M.N., Efthimiopoulos S., Shioi J., Robakis N.K.;
 RT "The chondroitin sulfate attachment site of appican is formed by
 RT splicing out exon 15 of the amyloid precursor gene.";
 RL J. Biol. Chem. 270:10388-10391(1995).
 RN [10]
 RP BETA-AMYLOID METAL-BINDING.
 RX MEDLINE=99316162; PubMed=10386999;
 RA Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,
 RA Scarpa R.C., Cuajungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,
 RA Bush A.I.;
 RT "The A beta peptide of Alzheimer's disease directly produces hydrogen
 RT peroxide through metal ion reduction.";
 RL Biochemistry 38:7609-7616(1999).
 RN [11]
 RP BETA-AMYLOID ZINC BINDING.
 RX MEDLINE=99343552; PubMed=10413512;
 RA Liu S.T., Howlett G., Barrow C.J.;
 RT "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
 RT of the A beta peptide of Alzheimer's disease.";
 RL Biochemistry 38:9373-9378(1999).
 RN [12]
 RP IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
 RP GLY-704.
 RX MEDLINE=21956095; PubMed=11959460;
 RA Kanski J., Varadarajan S., Aksenova M., Butterfield D.A.;
 RT "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
 RT peptide 1-42-associated oxidative stress and neurotoxicity.";
 RL Biochim. Biophys. Acta 1586:190-198(2001).
 RN [13]
 RP PHOSPHORYLATION.
 RX MEDLINE=97239592; PubMed=9085254;
 RA Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Gandy S.E.,
 RA Greengard P., Suzuki T.;
 RT "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
 RT phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and
 RT cultured cells.";
 RL Mol. Med. 3:111-123(1997).
 RN [14]

RP PHOSPHORYLATION ON SER-730.
 RX MEDLINE=99262094; PubMed=10329382;
 RA Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
 RA Greengard P., Nairn A.C., Suzuki T.;
 RT "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
 RT precursor protein at Ser655 by a novel protein kinase.";
 RL Biochem. Biophys. Res. Commun. 258:300-305(1999).
 RN [15]
 RP PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
 RP THR-743.
 RX MEDLINE=99274744; PubMed=10341243;
 RA Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,
 RA Kirino Y., Greengard P., Suzuki T.;
 RT "Role of phosphorylation of Alzheimer's amyloid precursor protein
 RT during neuronal differentiation.";
 RL J. Neurosci. 19:4421-4427(1999).
 RN [16]
 RP PHOSPHORYLATION ON THR-743.
 RX MEDLINE=20396183; PubMed=10936190;
 RA Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,
 RA Greengard P., Kirino Y., Nairn A.C., Suzuki T.;
 RT "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
 RT protein by cyclin-dependent kinase 5.";
 RL J. Neurochem. 75:1085-1091(2000).
 RN [17]
 RP CARBOHYDRATE STRUCTURE OF APPICAN.
 RX MEDLINE=21463085; PubMed=11479316;
 RA Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
 RA Sugahara K., Robakis N.K.;
 RT "Appican, the proteoglycan form of the amyloid precursor protein,
 RT contains chondroitin sulfate E in the repeating disaccharide region
 RT and 4-O-sulfated galactose in the linkage region.";
 RL J. Biol. Chem. 276:37155-37160(2001).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP. Inhibits
 CC G(O) alpha ATPase activity. Acts as a kinesin I membrane receptor,
 CC mediating the axonal transport of beta-secretase and presenilin 1
 CC (By similarity). May be involved in copper homeostasis/oxidative
 CC stress through copper ion reduction. Can regulate neurite
 CC outgrowth through binding to components of the extracellular
 CC matrix such as heparin and collagen I and IV (By similarity). The
 CC splice isoforms that contain the BPTI domain possess protease
 CC inhibitor activity (By similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
 CC only weakly transient metals and have little reducing activity due
 CC to substitutions of transient metal chelating residues. Beta-APP42
 CC may activate mononuclear phagocytes in the brain and elicit
 CC inflammatory responses. Promotes both tau aggregation and TPK II-
 CC mediated phosphorylation (By similarity).

CC -!- FUNCTION: Appicans elicit adhesion of neural cells to the
 CC extracellular matrix and may regulate neurite outgrowth in the
 CC brain.
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
 CC (via its TPR domains), APPBP2 (via BaSS) (By similarity) and DDB1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity). Interacts,
 CC through a C-terminal domain, with GNAO1. Amyloid beta-42 binds
 CC CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid
 CC associates with HADH2 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the

Query Match 97.0%; Score 3937; DB 1; Length 770;
 Best Local Similarity 96.9%; Pred. No. 9.1e-190;
 Matches 746; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Db	1	MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDSIDSADAEEDDSDVWWGGADTDYADGGEDKVVEVAEEEEVADVEEE	240
Qy	241	EADDDDEDDEGDVEVEEEAEEPVEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
		:	
Db	241	EAEDDEDVEDGDVEVEEEAEEPVEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSVSSQSLLKTTSEPLPQD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480

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Qy      481 QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      481 QAVPPRPHHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy      541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600

Qy      601 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 660
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy      661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      661 IKTEEISEVKMDAEFGHDSGFVVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy      721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMQN 770
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMQN 770

```

RESULT 6

A4_MOUSE

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ID      A4_MOUSE          STANDARD;          PRT;          770 AA.
AC      P12023; P97487; P97942; Q99K32;
DT      01-OCT-1989 (Rel. 12, Created)
DT      10-OCT-2003 (Rel. 42, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE      amyloid protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains:
DE      Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99
DE      (APP-C99); Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein
DE      40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase
DE      C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
DE      (APP-C59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)
DE      (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-CTF(50)
DE      (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain
DE      50) (AID(50)); C31].
GN      APP.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORM APP695).
RC      TISSUE=Brain;
RX      MEDLINE=88106489; PubMed=3322280;
RA      Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
RT      "Complementary DNA for the mouse homolog of the human amyloid beta
RT      protein precursor.";
RL      Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN      [2]
RP      REVISIONS.
RA      Yamada T.;
RL      Submitted (MAR-1988) to the EMBL/GenBank/DDBJ databases.
RN      [3]

```

RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=92096458; PubMed=1756177;
 RA de Strooper B., van Leuven F., van den Berghe H.;
 RT "The amyloid beta protein precursor or proteinase nexin II from mouse
 RT is closer related to its human homolog than previously reported.";
 RL Biochim. Biophys. Acta 1129:141-143(1991).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC STRAIN=SAMP8; TISSUE=Hippocampus;
 RX MEDLINE=21130647; PubMed=11235921;
 RA Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,
 RA Alvarez J., Morley J.E.;
 RT "Molecular cloning, expression, and regulation of hippocampal amyloid
 RT precursor protein of senescence accelerated mouse (SAMP8).";
 RL Biochem. Cell Biol. 79:57-67(2001).
 RN [5]
 RP SEQUENCE OF 1-19 FROM N.A.
 RX MEDLINE=92209998; PubMed=1555768;
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
 RA Sakai Y.;
 RT "Positive and negative regulatory elements for the expression of the
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
 RL Gene 112:189-195(1992).
 RN [6]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).
 RC TISSUE=Breast tumor;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Kidney;
 RX MEDLINE=89149813; PubMed=2493250;
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
 RT "Structure and expression of the alternatively-spliced forms of mRNA
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein
 RT precursor.";
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).

RN [8]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC STRAIN=CD-1; TISSUE=Placenta;
 RX MEDLINE=89345111; PubMed=2569710;
 RA Fukuchi K., Martin G.M., Deeb S.S.;
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
 precursor of *Mus domesticus*.";
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN [9]
 RP SEQUENCE OF 656-737 FROM N.A.
 RC STRAIN=129/Sv;
 RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capecchi M.,
 RA Loring J.F., Goate A.M.;
 RT "Introduction of six mutations into the mouse genome using 'Hit and
 Run' gene-targeting: introduction of familial Alzheimer's disease
 mutations into the mouse amyloid precursor protein gene and
 humanization of the A-beta fragment.";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
 RN [10]
 RP TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.
 RX MEDLINE=93287808; PubMed=8510506;
 RA Sola C., Mengod G., Ghetti B., Palacios J.M., Triarhou L.C.;
 RT "Regional distribution of the alternatively spliced isoforms of beta
 APP RNA transcript in the brain of normal, heterozygous and
 homozygous weaver mutant mice as revealed by in situ hybridization
 histochemistry.";
 RL Brain Res. Mol. Brain Res. 17:340-346(1993).
 RN [11]
 RP INTERACTION WITH KNS2.
 RX MEDLINE=21010507; PubMed=11144355;
 RA Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.;
 RT "Axonal transport of amyloid precursor protein is mediated by direct
 binding to the kinesin light chain subunit of kinesin-I.";
 RL Neuron 28:449-459(2000).
 RN [12]
 RP C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-728;
 RP THR-743; TYR-757; ASN-759 AND TYR-762.
 RX MEDLINE=21408156; PubMed=11517249;
 RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
 RA Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,
 RA Kyriakis J.M., Nishimoto I.;
 RT "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1
 scaffolds Alzheimer's amyloid precursor protein with JNK.";
 RL J. Neurosci. 21:6597-6607(2001).
 RN [13]
 RP INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.
 RX MEDLINE=22028091; PubMed=11912189;
 RA Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.;
 RT "Interaction of Alzheimer's beta-amyloid precursor family proteins
 with scaffold proteins of the JNK signaling cascade.";
 RL J. Biol. Chem. 277:20070-20078(2002).
 RN [14]
 RP INTERACTION OF CTF PEPTIDES WITH NUMB.
 RX MEDLINE=22008109; PubMed=12011466;
 RA Roncarati R., Sestan N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,
 RA Meucci O., McGlade J.C., Rakic P., D'Adamio L.;
 RT "The gamma-secretase-generated intracellular domain of beta-amyloid

RT precursor protein binds Numb and inhibits Notch signaling.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).
 RN [15]
 RP GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APBB1.
 RX MEDLINE=21437805; PubMed=11553691;
 RA Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.;
 RT "The amyloid precursor protein (APP)-cytoplasmic fragment generated by
 RT gamma-secretase is rapidly degraded but distributes partially in a
 RT nuclear fraction of neurones in culture.";
 RL J. Neurochem. 78:1168-1178(2001).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions. Can promote transcription activation through binding
 CC to APBB1/Tip60 and inhibit Notch signaling through interaction
 CC with Numb. Couples to apoptosis-inducing pathways such as those
 CC mediated by G(O) and JIP. Inhibits G(0) alpha ATPase activity (By
 CC similarity). Acts as a kinesin I membrane receptor, mediating the
 CC axonal transport of beta-secretase and presenilin 1. May be
 CC involved in copper homeostasis/oxidative stress through copper ion
 CC reduction. Can regulate neurite outgrowth through binding to
 CC components of the extracellular matrix such as heparin and
 CC collagen I and IV (By similarity). The splice isoforms that
 CC contain the BPTI domain possess protease inhibitor activity (By
 CC similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
 CC only weakly transient metals and have little reducing activity due
 CC to substitutions of transient metal chelating residues. Beta-APP42
 CC may activate mononuclear phagocytes in the brain and elicit
 CC inflammatory responses. Promotes both tau aggregation and TPK II-
 CC mediated phosphorylation (By similarity).
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis.
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits
 CC its serine phosphorylation. Also interacts with GPCR-like protein
 CC BPP, FPRL1, APPBP1, IB1, KNS2 (via its TPR domains), APPBP2 (via
 CC BaSS) and DDB1 (By similarity). In vitro, it binds MAPT via the
 CC MT-binding domains (By similarity). Associates with microtubules
 CC in the presence of ATP and in a kinesin-dependent manner (By
 CC similarity). Interacts, through a C-terminal domain, with GNAO1
 CC (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal
 CC neurons (By similarity). Beta-amyloid associates with HADH2 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete

Query Match 96.7%; Score 3923; DB 1; Length 770;
 Best Local Similarity 96.6%; Pred. No. 4.6e-189;
 Matches 744; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

[illegible]

AC Q95241;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
 DE protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
 DE APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
 DE Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
 DE CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DE secretase C-terminal fragment 50); C31].
 GN APP.
 OS Saimiri sciureus (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
 OX NCBI_TaxID=9521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney, and Liver;
 RX MEDLINE=96108492; PubMed=8532114;
 RA Levy E., Amorim A., Frangione B., Walker L.C.;
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with
 RT cerebral amyloid angiopathy."
 RL Neurobiol. Aging 16:805-808(1995).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction. In vitro, copper-metallated APP induces neuronal
 CC death directly or is potentiated through Cu(II)-mediated low-
 CC density lipoprotein oxidation (By similarity). Can regulate
 CC neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
 CC (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP

CC and in a kinesin-dependent manner (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized to endosomes and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
 CC and nuclei of neurons (By similarity).

CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=APP770;
 CC IsoId=Q95241-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=Q95241-2; Sequence=Not described;

CC -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).

CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).

CC -!- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 CC similarity).

CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).

CC -!- PTM: N- and O-glycosylated (By similarity).

CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).

CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and

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CC      inhibits collagen-binding (By similarity).
CC      -!- SIMILARITY: Belongs to the APP family.
CC      -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; S81024; AAD14347.1; -.
DR      HSSP; P05067; 1AAP.
DR      InterPro; IPR008155; A4_APP.
DR      InterPro; IPR008154; A4_extra.
DR      InterPro; IPR001255; Beta-APP.
DR      InterPro; IPR002223; Kunitz_BPTI.
DR      Pfam; PF02177; A4_EXTRA; 1.
DR      Pfam; PF03494; Beta-APP; 1.
DR      Pfam; PF00014; Kunitz_BPTI; 1.
DR      PRINTS; PR00203; AMYLOIDA4.
DR      PRINTS; PR00759; BASICPTASE.
DR      ProDom; PD000222; Kunitz_BPTI; 1.
DR      SMART; SM00006; A4_EXTRA; 1.
DR      SMART; SM00131; KU; 1.
DR      PROSITE; PS00319; A4_EXTRA; 1.
DR      PROSITE; PS00320; A4_INTRA; 1.
DR      PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR      PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW      Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW      Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW      Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW      Proteoglycan; Amyloid; Alternative splicing.
FT      SIGNAL          1      17      BY SIMILARITY.
FT      CHAIN           18      751      A4 PROTEIN.
FT      CHAIN           18      668      SOLUBLE APP-ALPHA (POTENTIAL).
FT      CHAIN           18      652      SOLUBLE APP-BETA (POTENTIAL).
FT      CHAIN          653      751      C99 (POTENTIAL).
FT      CHAIN          653      694      BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT      CHAIN          653      692      BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT      CHAIN          669      751      C83 (POTENTIAL).
FT      CHAIN          669      694      P3(42) (POTENTIAL).
FT      CHAIN          669      692      P3(40) (POTENTIAL).
FT      CHAIN          693      751      GAMMA-CTF(59) (POTENTIAL).
FT      CHAIN          695      751      GAMMA-CTF(57) (POTENTIAL).
FT      CHAIN          702      751      GAMMA-CTF(50) (POTENTIAL).
FT      CHAIN          721      751      C31 (POTENTIAL).
FT      DOMAIN          18      680      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM        681      704      POTENTIAL.
FT      DOMAIN          705      751      CYTOPLASMIC (POTENTIAL).
FT      DOMAIN          96      110      HEPARIN-BINDING (BY SIMILARITY).
FT      DOMAIN         181      188      ZINC-BINDING (BY SIMILARITY).
FT      DOMAIN         291      341      BPTI/KUNITZ INHIBITOR.
FT      DOMAIN         316      344      HEPARIN-BINDING (BY SIMILARITY).
FT      DOMAIN         363      428      HEPARIN-BINDING (BY SIMILARITY).
FT      DOMAIN         504      521      COLLAGEN-BINDING (BY SIMILARITY).

```


FT	DOMAIN	713	732	INTERACTION WITH G(O)-ALPHA
FT				(BY SIMILARITY).
FT	DOMAIN	230	260	ASP/GLU-RICH (ACIDIC).
FT	DOMAIN	274	280	POLY-THR.
FT	SITE	144	144	REQUIRED FOR COPPER(II) REDUCTION
FT				(BY SIMILARITY).
FT	ACT_SITE	301	302	REACTIVE BOND.
FT	SITE	652	653	CLEAVAGE (BY BETA-SECRETASE)
FT				(BY SIMILARITY).
FT	SITE	653	654	CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT	SITE	668	669	CLEAVAGE (BY ALPHA-SECRETASE)
FT				(BY SIMILARITY).
FT	SITE	685	685	INVOLVED IN FREE RADICAL PROPAGATION
FT				(BY SIMILARITY).
FT	SITE	687	687	INVOLVED IN OXIDATIVE REACTIONS
FT				(BY SIMILARITY).
FT	SITE	692	693	CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT				(BY SIMILARITY).
FT	SITE	694	695	CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT				(BY SIMILARITY).
FT	SITE	701	702	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT				(BY SIMILARITY).
FT	SITE	705	715	BASOLATERAL SORTING SIGNAL
FT				(BY SIMILARITY).
FT	SITE	720	721	CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
FT				(BY SIMILARITY).
FT	SITE	738	741	ENDOCYTOSIS SIGNAL.
FT	SITE	740	743	NPXY MOTIF.

Query Match 96.6%; Score 3921.5; DB 1; Length 751;
 Best Local Similarity 96.9%; Pred. No. 5.3e-189;
 Matches 746; Conservative 2; Mismatches 3; Indels 19; Gaps 1;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRDRKQCKTHPHIVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLP CGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLP CGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
		:	
Db	181	GVEFVCCPLAEESDHVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSV-----	344

Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
		:	
Db	345	---IPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	401
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	402	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	461
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	462	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	521
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Db	522	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	581
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	582	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	641
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVVATVIVITL	720
Db	642	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVVATVIVITL	701
Qy	721	VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	702	VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	751

RESULT 8

A4_TETFL

ID A4_TETFL STANDARD; PRT; 780 AA.

AC 073683;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog precursor [Contains:

DE Beta-amyloid protein (Beta-APP) (A-beta)].

GN APP.

OS Tetraodon fluviatilis (Puffer fish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

OC Tetraodontidae; Tetraodontidae; Tetraodon.

OX NCBI_TaxID=47145;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98252138; PubMed=9599080;

RA Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;

RT "Analysis of pufferfish homologues of the AT-rich human APP gene.";

RL Gene 210:17-24(1998).

CC -!- FUNCTION: Functional neuronal receptor which couples to

CC intracellular signaling pathway through the GTP-binding protein

CC G(O) (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Belongs to the APP family.

CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.


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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF018165; AAC41275.1; -.
DR HSSP; P05067; 1HZ3.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; FALSE_NEG.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW Serine protease inhibitor.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 780 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT HOMOLOG.
FT CHAIN 682 724 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN 19 711 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 712 732 POTENTIAL.
FT DOMAIN 733 780 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 323 382 BPTI/KUNITZ INHIBITOR.
FT SITE 769 772 CLATHRIN-BINDING (BY SIMILARITY).
FT DISULFID 327 378 BY SIMILARITY.
FT DISULFID 336 361 BY SIMILARITY.
FT CARBOHYD 560 560 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 780 AA; 88238 MW; 60071BE94520191D CRC64;

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Query Match 68.1%; Score 2763.5; DB 1; Length 780;
Best Local Similarity 67.4%; Pred. No. 4.1e-131;
Matches 541; Conservative 80; Mismatches 113; Indels 69; Gaps 11;

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Qy 7 LLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGKTCTCIDTK 66
   |||:| : | |||| : |||||:||||:||||:||||: |||||:| |
Db 8 LLLVAAASTLAAEVPTDVSMGLLAEPQVAMFCGKINMHINVQSGKWEPPDPSGKSCIGTK 67

Qy 67 EGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDA 126
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 68 EGILQYCQEVYPELQITNVVEANQPVSIQNWCKKGRKQCRSHMHIVVPYRCLVGEFVSDA 127

Qy 127 LLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVC 186
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

Db	128	LLVPDKCKFLHQERMNQCESHLHWHTVAKESCGDRAMNLHDYGMLLPCGIDRFRGVEFVC	187
Qy	187	CPLAEESDNVDSADAEEDSDVWWGGADTDYADGS-----EDKVVEVAEEE	232
		: : : :	
Db	188	CP-AEAERDMDSTEKDADSDVWWGGADNDYSDNSMVREPEPAEQQEETRPSVVEEEEG	246
Qy	233	EVAEVEEEE-----ADDEDEDEDGDEVEEEAEEPVEEATERTTSIA	273
		: : : : : :	
Db	247	EVAQEDDEEEEEEVLDTDQDGDGEEDHEAADDEEEEDVDEIDAFGESDDVDADEPTTNVA	306
Qy	274	---TTTTTTTESVEEVVREVCSEQAETGPCRAMISRWFYFDVTEGKCA-PFFYGGCGGNRN	329
		: : : :	
Db	307	MTTTTTTTTTTESVEEVVRMFCWAHADTGPCTASMPSWYFDAVDGRTMYELMYGGCGGNMN	366
Qy	330	NFDTEEYCMVCGSAMSQSLLKTTQEPLARDPVKLPPTAASTPDAVDKYLETPGDENEHA	389
		: : : :	
Db	367	NFESEYCLSVCSV-----VPTDMPSSPDAVDHYLETPADENEHA	407
Qy	390	HFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANE	449
		: : :	
Db	408	HFQKAKESLEAKHRERMSQVMREWEEAERQAKNLPKADKKIVIQRFQEKVEALEQEAASE	467
Qy	450	RQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTL	509
		: : :	
Db	468	RQQLVETHMARVEALLNDRRLALENYLTALQQDPPRPRHVFSLKKYVRAEQKDRQHTL	527
Qy	510	KHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLYNVPAVAEEIQDEVDELLQKE	569
		: : : :	
Db	528	KHFEHVRMVDPKKAAQIRPQVLTHLRVIEERMNQSLGLLYKVPGVADDIQDQV-ELLQRE	586
Qy	570	QNYSDDLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSLDDLQPDWH--SFGAD	627
		: : : : : :	
Db	587	QAEMAQQLANLQTDVRVSYGNDAIMPQELGDGQADLLP--QEDTLGGVGFVHPESFN--	642
Qy	628	SVPANTENEVEPVDPARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQK	687
		: : : : : : : : :	
Db	643	--QLNTENQVEPVDSRPTFERGVPTRP---VTGKSMEAVPELRMETEDRQSTEYEVHHQK	697
Qy	688	LVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVEVDAAVTPEER	747
		: :	
Db	698	LVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLRKKQYTSIHGGIIEVDAAVTPEER	757
Qy	748	HLSKMQQNGYENPTYKFFEQQMN	770
Db	758	HLSKMQQNGYENPTYKFFEQQMN	780

RESULT 9

A4_FUGRU

ID A4_FUGRU STANDARD; PRT; 737 AA.

AC O93279;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog precursor [Contains:

DE Beta-amyloid protein (Beta-APP) (A-beta)].

GN APP.

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetradontoidea; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98252138; PubMed=9599080;
 RA Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;
 RT "Analysis of pufferfish homologues of the AT-rich human APP gene."
 RL Gene 210:17-24(1998).
 CC -!- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the APP family.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF090120; AAD13392.1; -.
 DR HSSP; P05067; 1HZ3.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; FALSE_NEG.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
 KW Serine protease inhibitor.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 737 ALZHEIMER'S DISEASE AMYLOID A4
 FT PROTEIN HOMOLOG.
 FT CHAIN 639 681 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN 19 668 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 669 689 POTENTIAL.
 FT DOMAIN 690 737 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 286 344 BPTI/KUNITZ INHIBITOR.
 FT SITE 726 729 CLATHRIN-BINDING (BY SIMILARITY).
 FT ACT_SITE 300 301 REACTIVE BOND.

FT DISULFID 290 340 BY SIMILARITY.
FT DISULFID 299 323 BY SIMILARITY.
FT DISULFID 315 336 BY SIMILARITY.
FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 737 AA; 82856 MW; 6FAD01E2E3B2B7E2 CRC64;

Query Match 66.5%; Score 2699; DB 1; Length 737;
Best Local Similarity 67.2%; Pred. No. 6.4e-128;
Matches 519; Conservative 93; Mismatches 110; Indels 50; Gaps 12;

Qy 7 LLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGKTCTIDTK 66
: ||| | : | : | | | | | : | | | : | | | | : | | | | : | : | |
Db 8 VLLLVATLTRSSEIPADDTVGLLTPQVAMFCGKLNMHINVQNGKWESDPSGKTKSCLNTK 67

Qy 67 EGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDA 126
| | | | | | | | | | | | | | | : | | | | : | | | | : | | | | | | | | | |
Db 68 EGILQYCQEVYPELQITNVVEANQPVSIQNWCKKGRKQCRSHTHIVVPYRCLVGEFVSDA 127

Qy 127 LLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVFEFVC 186
| | | | | | | | | | : | | : | | | | | | | : | : | | | | | | | | | | | |
Db 128 LLVPDKCKFLHQERMNQCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVKFVC 187

Qy 187 CPLAEESDNVDSADAEEDSDVWWGGADTDYADGS---EDKVVEVAEEEEVAEVEEEEEAD 243
| | | | : | : | : | | | | | : | : | : | : | : | : | : | : |
Db 188 CP-AETEQETDSSEVEGEESDVWWGGADPEYSENSPPTPSRATYVAGD---AFERDENG 243

Qy 244 DDEDEDGDEVEEEAEPEYEEATERTTSIA--TTTTTTTESVEEVVREVCSEQAETGPCR 301
| | : | | : : | : | : | | : : | | | | | | | | | | | | | | | | | | | |
Db 244 GDEDEEDEDVDPTDE---QESDERTANVAMTTTTTTTTTESVEEVVRAVCWAQAESGPCR 300

Qy 302 AMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARDP 361
| | : | | | : : : | | : | | | | | | | | : | | | | : | | | | : | :
Db 301 AMLERWYFNPKKRRCVPFLFGGCGGNRNNFESEEEYCLAVCSSS----- 343

Qy 362 VKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAK 421
| | | | | | | | | : | | | | : | | | | : | | | | | | | | | | | | | | | |
Db 344 --LPTVAPSPDAVDQYFEAPGDDNEHADFRKAKESLEAKHRERMSQVMREWEEAERQAK 401

Qy 422 NLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQ 481
| | : | | | | | | | | : | | | | | | | | | : | | | | | | : | | |
Db 402 NLPRADKKAVIQHFQEKVEALEQEAAAGERQQLVETHMARVEALLNSRRRLTLENYLGALQ 461

Qy 482 AVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERM 541
| | | | | : : | | | | | | | | | : | | | | | | | | | | | | | | | |
Db 462 ANPPRARQVLSLLKKYVRAEQKDRQHTLKHVEHVRTVDPKAAQIRPQVLTHLRVIDERM 521

Qy 542 NQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDLANMIS---EPRI SYGNDALMPSLT 598
| | | : | | | | : | | | : : : : : : : : : : | | | | | | | |
Db 522 NQSLALLYKVPSVASEIQNQIYPAAGSD---CKDPVEHCVCPCQVDGLVSYGNDALMPDQA 578

Qy 599 ETKTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGL 658
: : : : | : | | | | | | | | | | | | | | | | | | :
Db 579 YSSAPMD-MGVDGLGSID-----QSFN----QANTENHVEPVDARPI PDRGLPTRP---V 625

Qy 659 TNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVI 718
: : : | | : | : : : | : | | | : | | | | | | | | | | | | | | | | |
Db 626 SSLKLEEMPEVRTETDKRQSAGYEVYHQKLVFFADDVGSNKGAIIGLMVGGVVIATVIVI 685

Qy 719 TLVMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
 |||||:|||||:|||||:|||||:|||||
 Db 686 TLVMLRKKQYTSIHGVEVDAAVTPEERHLARMQQNGYENPTYKFFEQMQN 737

RESULT 10

APP2_HUMAN

ID APP2_HUMAN STANDARD; PRT; 763 AA.
 AC Q06481;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Amyloid-like protein 2 precursor (Amyloid protein homolog) (APPH)
 DE (CDEI-box binding protein) (CDEBP).
 GN APLP2 OR APPL2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=93250009; PubMed=8485127;
 RA Sprecher C.A., Grant F.J., Grimm G., O'Hara P.J., Norris F.,
 RA Norris K., Foster D.C.;
 RT "Molecular cloning of the cDNA for a human amyloid precursor protein
 RT homolog: evidence for a multigene family.";
 RL Biochemistry 32:4481-4486(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=95217334; PubMed=7702756;
 RA von der Kammer H., Hanes J., Klaudiny J., Scheit K.H.;
 RT "A human amyloid precursor-like protein is highly homologous to a
 RT mouse sequence-specific DNA-binding protein.";
 RL DNA Cell Biol. 13:1137-1143(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=94035131; PubMed=8220435;
 RA Wasco W., Gurubhagavatula S., Paradis M., Romano D.M., Sisodia S.S.,
 RA Hyman B.T., Neve R.L., Tanzi R.E.;
 RT "Isolation and characterization of APLP2 encoding a homologue of the
 RT Alzheimer's associated amyloid beta protein precursor.";
 RL Nat. Genet. 5:95-99(1993).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: May play a role in the regulation of hemostasis. The
 CC soluble form may have inhibitory properties towards coagulation
 CC factors. May interact with cellular G-protein signaling pathways.
 CC May bind to the DNA 5'-GTCACATG-3'(CDEI box).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein and nuclear
 CC (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=Q06481-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q06481-2; Sequence=VSP_000018;
 CC Name=3;
 CC IsoId=Q06481-3; Sequence=VSP_000019;
 CC -!- TISSUE SPECIFICITY: In placenta, brain, heart, lung, liver, kidney
 CC and endothelial tissues.
 CC -!- SIMILARITY: Belongs to the APP family.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
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 CC -----
 DR EMBL; S60099; AAC60589.1; -.
 DR EMBL; L09209; AAA35526.1; -.
 DR EMBL; Z22572; CAA80295.1; -.
 DR EMBL; L27631; AAC41701.1; -.
 DR EMBL; BC000373; AAH00373.1; -.
 DR PIR; A49321; A49321.
 DR HSSP; P05067; 1MWP.
 DR Genew; HGNC:598; APLP2.
 DR MIM; 104776; -.
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0003677; F:DNA binding; NAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; NAS.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR002223; Kunitz_BPTI.

DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Transmembrane; Signal; Alternative splicing; DNA-binding;
 KW Nuclear protein; Serine protease inhibitor.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 763 AMYLOID-LIKE PROTEIN 2.
 FT DOMAIN 30 692 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 693 716 POTENTIAL.
 FT DOMAIN 717 763 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 215 280 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT DOMAIN 306 364 BPTI/KUNITZ INHIBITOR.
 FT DOMAIN 215 231 POLY-GLU.
 FT ACT_SITE 320 321 REACTIVE BOND (BY SIMILARITY).
 FT DISULFID 310 360 BY SIMILARITY.
 FT DISULFID 319 343 BY SIMILARITY.
 FT DISULFID 335 356 BY SIMILARITY.
 FT VARSPLIC 308 363 Missing (in isoform 2).
 FT /FTId=VSP_000018.
 FT VARSPLIC 613 624 Missing (in isoform 3).
 FT /FTId=VSP_000019.
 FT CONFLICT 543 543 S -> I (IN REF. 1).
 SQ SEQUENCE 763 AA; 86955 MW; CA3A7D6DDB8A28D0 CRC64;

Query Match 48.8%; Score 1981.5; DB 1; Length 763;
 Best Local Similarity 50.4%; Pred. No. 4.8e-92;
 Matches 408; Conservative 127; Mismatches 168; Indels 107; Gaps 21;

Qy 5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDF 56
 | |||| || || : ||| :|||||||:||||:|:| |||: ||
 Db 15 LLLLLLVGLTAPALALAGYIEALAANAGTGFVAEPQIAMFCGKLNMHVNIQTGKWEPPD 74

 Qy 57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
 :|||:| :||| :|||||:|||||||:|||| |::| |||:| :|||: || |::
 Db 75 TGTKSCFETKEEVQLQYCQEMYPELQITNVMEANQRVSIDNWCRRDKKQCKS--RFVTPFK 132

 Qy 117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
 ||||| ||||:||:| |:|||:||| | |||| || | : |: |||||:|
 Db 133 CLVGEFVSDVLLVPEKCFHFKERMEVCENHQHWHTVVKACLTQGMTLYSYGMLLPCGV 192

 Qy 177 DKFRGVFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAE 236
 |:| | |:||| : :| : |||: : : | || | :| |:
 Db 193 DQFHGTEYVCCPQTKIIGSVSKEEEEEDEE-----EEEEDEEEDYDVYKSEFPTEAD 245

 Qy 237 VEE--EEA--DDDEDDGDEVEEEAE-----EPYEEATERTTSIATTTTTTTESVE 284
 :|: | | :||||:|:|:| |: : : | | | : | : :
 Db 246 LEDFTEAAVDEDDDEEEGEEVVEDRDYYYDTFKGDDYNE--ENPTEPGSDGTMSDKEIT 303

 Qy 285 EVVREVCSEQAETGPCRAMISRWFYDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSA 344


```

      | : ||| : | ||||| : : ||||| : : ||| | ||||| ||||| : : ||||| :
Db      304 HDVKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMVCKAM 363
Qy      345 MSQSLLKTTQEPLARDPVKLPPTAASTPDAVDKYLET PGDENEHAHFQKAKERLEAKHRE 404
      :      | ||| : || | || | : |||| ||||| : || : ||
Db      364 I-----PPTPLPT-----NDVDVYFETSADDNEHARFQKAKEQLEIRHRN 403
Qy      405 RMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAM 464
      || : | : ||||| ||||| : : : |||| | : || : || : || : || : || : ||
Db      404 RMDRVKKEWEEAELQAKNLPKAERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAM 463
Qy      465 LNDRRRLALENYITALQAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAA 524
      ||||| : ||||| : ||| : |||| : | : ||||| ||| || : || : || ||| : |||
Db      464 LNDRRRMALENYLAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAA 523
Qy      525 QIRSQVMTHLRVIYERMNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDVLANMISEP 584
      | : ||||| || || ||||| || || : || : || : || : || : || : || : ||
Db      524 QMKSQVMTHLHVIEERNQSLSLLYKVPYVAQEIQEEIDELLQEQR-----ADM---- 572
Qy      585 RISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARP 644
      | : ||| | : | | : : || : | | || | | : |
Db      573 -----DQFTASISETPVDVR---VSSEES-EEIPPFHPF--HPFPALPENE----DTQP 616
Qy      645 AADRGLTTRPGSGLTN-----IKTEE---ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVG 696
      : : ||| : | || | : | : | | : | : : : | || |
Db      617 ELYHPM--KKGSVGGEQDGGGLIGAEKVINSKNKVDENMVIDETLDV--KEMIFNAERVG 672
Qy      697 S-----NKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGVEVD 739
      : | : ||| : | ||||| : |||| : ||| : | || : |||
Db      673 GLEERESVGPLREDFSLSSALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVD 732
Qy      740 AAVTPEERHLSKMQQNGYENPTYKFFEQQMQ 769
      : ||||| : ||| : ||||| : ||||
Db      733 PMLTPEERHLNKMQNHGYENPTYKYLEQQMQ 762

```

RESULT 11

APP2_RAT

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ID APP2_RAT          STANDARD;          PRT;      765 AA.
AC P15943;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Amyloid-like protein 2 precursor (Sperm membrane protein YWK-II).
GN APLP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 1-627 FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain, and Heart;
RX MEDLINE=94368849; PubMed=8086458;
RA Sandbrink R., Masters C.L., Beyreuther K.;
RT "Complete nucleotide and deduced amino acid sequence of rat amyloid
RT protein precursor-like protein 2 (APLP2/APPH): two amino acids length
RT difference to human and murine homologues.";

```

RL Biochim. Biophys. Acta 1219:167-170(1994).
 RN [2]
 RP SEQUENCE OF 575-765 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=90207205; PubMed=1690887;
 RA Yan Y.C., Bai Y., Wang L.F., Miao S.Y., Koide S.S.;
 RT "Characterization of cDNA encoding a human sperm membrane protein
 RT related to A4 amyloid protein."
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2405-2408(1990).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=A;
 CC IsoId=P15943-1; Sequence=Displayed;
 CC Name=B;
 CC IsoId=P15943-2; Sequence=VSP_000021;
 CC Name=C;
 CC IsoId=P15943-3; Sequence=VSP_000020;
 CC Name=D;
 CC IsoId=P15943-4; Sequence=VSP_000020, VSP_000021;
 CC -!- SIMILARITY: Belongs to the APP family.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
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 CC -----
 DR EMBL; X77934; CAA54906.1; -.
 DR EMBL; M31322; AAA42352.1; -.
 DR PIR; A35981; A35981.
 DR PIR; S42880; S42880.
 DR HSSP; P05067; 1MWP.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Transmembrane; Alternative splicing; Serine protease inhibitor;
 KW Signal; Glycoprotein.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 765 AMYLOID-LIKE PROTEIN 2.
 FT DOMAIN 30 695 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 696 718 POTENTIAL.
 FT DOMAIN 719 765 CYTOPLASMIC (POTENTIAL).

FT	DOMAIN	218	282	ASP/GLU-RICH (HIGHLY ACIDIC).
FT	DOMAIN	308	366	BPTI/KUNITZ INHIBITOR.
FT	ACT_SITE	322	323	REACTIVE BOND (BY SIMILARITY).
FT	DISULFID	312	362	BY SIMILARITY.
FT	DISULFID	321	345	BY SIMILARITY.
FT	DISULFID	337	358	BY SIMILARITY.
FT	DOMAIN	218	229	POLY-GLU.
FT	CARBOHYD	628	628	O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT	VARSPPLIC	311	365	Missing (in isoform C and isoform D). /FTId=VSP_000020.
FT	VARSPPLIC	616	627	Missing (in isoform B and isoform D). /FTId=VSP_000021.
FT	CONFLICT	575	577	DQF -> EFV (IN REF. 2).
SQ	SEQUENCE	765 AA;	86882 MW;	CF51FCCCE305A0CF CRC64;

Qy	5	LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP	56
		: : : : : : :	
Db	15	LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPP	74
Qy	57	SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR	116
		: : : : : : : : : : :	
Db	75	TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKKQCRS--HIVIPFK	132
Qy	117	CLVGFEVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI	176
		: : : : : :	
Db	133	CLVGFEVSDVLLVPENCQFFHQERMEVCEKHQRWHTVVKEACLTEGMTLYSYGMLLPCGV	192
Qy	177	DKFRGVEFVCCPLAE--ESDNVDSADAEEDDSVWVGADTDYA-DGSEDKVVEVAEEEE	233
		: : : : : : : : : :	
Db	193	DQFHGTEYVCCPQTKVVDSDSTMSKEEEEEEEEE-----DEEDYALDKSEFPTEADLEDFT	248
Qy	234	VAEVEEEEEADDDDEDDGDEVEEEAEPEYEE-----ATERTTSIATTTTTTTESVEEVV	287
		: : : : : : : : : : : : : : : :	
Db	249	EAAADEDEDEEEEEEEEEEGEEVVEDRDYYYDSFKGDDYNEENPTEPSSDGTISDKEIAHDV	308
Qy	288	REVCSEQAETGPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQ	347
		: : : : : : : : : :	
Db	309	KAVCSQEAMTGPCRAVMRWFYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMVCKTMI--	366
Qy	348	SLLKTTQEPLARDPVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMS	407
		: : : :	
Db	367	-----PPTPLPT-----NDVDVYFETSADDNEHARFQKAKEQLEIRHRSRMD	408
Qy	408	QVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLND	467
		: : : : : : : : : :	
Db	409	RVKKEWEEAELQAKNLPKAERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLND	468
Qy	468	RRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIR	527
		: : : : : : : : : : :	
Db	469	RRRIALENYLAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMK	528
Qy	528	SQVMTHLRVIYERMNQSLSLLYNPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRIS	587
		: : : : : :	

Db	529	SQVMTHLHVIEERRNQSLSLLYKVPYVAQEIQEEIDELLQEQR-----ADM-----	574
Qy	588	YGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAAD	647
		:: :: :: :: :: :: :: :: :: :: :: ::	
Db	575	---DQFTSSISENPVDVR---VSSEES-EEIPPFHPF--HPFPSLSENE----DTQPELY	621
Qy	648	RGLTTRPGSGLTN-----IKTEE--ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS--	697
		: : : :: :: :: :: :: :: :: :: ::	
Db	622	HPM--KKGSGMAEQDGGLIGAEKVINSKNKM DENMVIDETLDV--KEMIFNAERVGGLE	677
Qy	698	-----NKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIH HGVVEVDAAV	742
		: :: :: :: :: :: :: :: :: ::	
Db	678	EEPDSVGPLREDFSLSSSALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVHPML	737
Qy	743	TPEERHLSKMQQNGYENPTYKFFEQMQ	769
		:: :: ::	
Db	738	TPEERHLNKM ONHGYENPTYKYLEOMO	764

APP2 MOUSE

AC 006335;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Amyloid-like protein 2 precursor (CDEI-box binding protein) (CDEBP).

GN APLP2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Fetal brain;

RA von der Kammer H.;

RL Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE OF 1-246 FROM N.A.

RX MEDLINE=94032480; PubMed=8218408;

RA Hanes J., von der Kammer H., Kristjansson G.I., Scheit K.H.;

RT "The complete cDNA coding sequence for the mouse CDEI binding

RT protein.";

RL Biochim. Biophys. Acta 1216:154-156(1993).

RN [3]

RP SEQUENCE OF 185-695 FROM N.A.

RC STRAIN=BALB/c; TISSUE=Heart;

RX MEDLINE=93129193; PubMed=1482349;

RA Vidal F., Blangy A., Rassoulzadegan M., Cuzin F.;

RT "A murine sequence-specific DNA binding protein shows extensive local

RT similarities to the amyloid precursor protein.";

RL Biochem. Biophys. Res. Commun. 189:1336-1341 (1992).

RN [4]

RP SEQUENCE OF 1-35 FROM N.A.

RC STRAIN=129/Sv;

RX MEDLINE=96029629; PubMed=7592716;

RA Gilbert D.J., Jenkins N.A., Sisodia S.S.;
 RT "The mouse APLP2 gene. Chromosomal localization and promoter
 RT characterization.";
 RL J. Biol. Chem. 270:25475-25480(1995).
 CC -!- FUNCTION: Binds to the DNA 5'-GTCACATG-3' (CDEI box) which plays
 CC an important role in the early development of embryos.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein and nuclear
 CC (Potential).
 CC -!- SIMILARITY: Belongs to the APP family.
 CC -----
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 CC -----
 DR EMBL; Z22592; CAA80306.1; -.
 DR EMBL; M97216; AAA20039.1; -.
 DR EMBL; U34291; AAC52318.1; -.
 DR PIR; JC1404; JC1404.
 DR PIR; S38344; S38344.
 DR HSSP; P05067; 1MWP.
 DR MGD; MGI:88047; Aplp2.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 KW Transmembrane; DNA-binding; Signal; Nuclear protein.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 695 AMYLOID-LIKE PROTEIN 2.
 FT DOMAIN 30 624 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 625 648 POTENTIAL.
 FT DOMAIN 649 695 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 218 294 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT DOMAIN 218 231 POLY-GLU.
 FT DOMAIN 256 266 POLY-GLU.
 FT CARBOHYD 485 485 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 185 189 GMLLP -> MACCC (IN REF. 3).
 SQ SEQUENCE 695 AA; 78944 MW; BBF4B95AAB2A0311 CRC64;

Query Match 42.0%; Score 1704.5; DB 1; Length 695;
 Best Local Similarity 46.9%; Pred. No. 3e-78;
 Matches 371; Conservative 113; Mismatches 170; Indels 137; Gaps 24;

Qy 5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
 | :||| ||| : ||| :||| ||| |||:||||:|:| |||: ||
 Db 15 LLVLLLGLTAPAAALAGYIEALAANAGTGFVAEAPQIAMLCGKLNMHVNIQTGKWEPPD 74
 Qy 57 SGTCTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
 :|||:|: ||| :||| |||:|||||:||||| |||:|: |||: | |||:
 Db 75 TGTKSCLGTKEEVLYCQEIYPELQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK 132

Qy	117	CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI	176
		: : : : : :	
Db	133	CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSYGMLLPCGV	192
Qy	177	DKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAE	236
		: : : : :	
Db	193	DQFHGTEYVCCP---QTKTVDS-----DSTMSK-----EEEE---	221
Qy	237	VEEEEADDDDEDEDGDEVVEEEAEEPYYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAE	296
		: : : : : : :	
Db	222	-EEEEDEEDEEDYDLDKSEFPTEADLEDLTE---AAADEEEEEDEEEEGEEVVED-----	270
Qy	297	TGPCRAMISRWFYFDVTEGKCAPPFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEP	356
		: : : : : : :	
Db	271	-----RDYYYD-----PF----KGDDYNEENPTE-----PSSEGTI--SDKE	301
Qy	357	LARDPVKLPPTTAASTPDVDKYLETPGDENEHAFQKAKERLEAKHRERMSQVMREWEEA	416
		: : : : :	
Db	302	IVHD-VKVPPTPLPTND-VDVYLETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEA	359
Qy	417	ERQAKNLPKADKKAVIQHFQEKVESLEQEAAANERQQQLVETHMARVEAMLNDRRRRLALENY	476
		: : : : : : : : : : : : :	
Db	360	ELQAKNLPKTERQTLIQHFAQAMVKALEKEAASEKQQQLVETHLARVEAMLNDRRRRIALENY	419
Qy	477	ITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRV	536
		: : : : : : :	
Db	420	LAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHV	479
Qy	537	IYERMNQSLSLLYNPVPAVAEEIQDEVDELLOKEQNYSDDVLANMISEPRI SYGNDALMP	596
		: : : : : : :	
Db	480	IEERNQSLTLTYKVPYVAQEIQEEIDELLQEQR-----ADM-----DQFTSS	522
Qy	597	LTETKTTVELLPVNGEFSDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGS	656
		: : : : : : : : : :	
Db	523	ISENPVDVRVSSEESE-EIPPFHPLHPF-----PSLSENE-----GSGMAEQDG-	565
Qy	657	GLTNIKTEEI-SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS-----N	698
		: : : : : : : :	
Db	566	GLIGAEKVINSKNKMDENMVIDETLDV--KEMIFNAERVGGLEEPE SVGPLRED FSL	623
Qy	699	KGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVEVDAAVTPEERHL SKMQQNGYE	758
		: : : : : : :	
Db	624	SNALIGLLVIAVAIATVIVISLVMLRKRYGTISHGIVEVDPMLTPEERHLNKMQN HGYE	683
Qy	759	NPTYKFFE QMQ	769
		:	
Db	684	NPTYKYLEOMO	694

GN APLP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98088960; PubMed=9428684;
 RA Paliga K., Peraus G., Kreger S., Duwrrwang U., Hesse L., Multhaup G.,
 RA Masters C.L., Beyreuther K., Weidemann A.;
 RT "Human amyloid precursor-like protein 1 -- cDNA cloning, ectopic
 RT expression in COS-7 cells and identification of soluble forms in the
 RT cerebrospinal fluid.";
 RL Eur. J. Biochem. 250:354-363(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98180887; PubMed=9521588;
 RA Lenkkeri U., Kestila M., Lamerdin J., McCready P., Adamson A.,
 RA Olsen A., Tryggvason K.;
 RT "Structure of the human amyloid-precursor-like protein gene APLP1 at
 RT 19q13.1.";
 RL Hum. Genet. 102:192-196(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP POSSIBLE FUNCTION, AND TISSUE SPECIFICITY.
 RX MEDLINE=96115107; PubMed=7494461;
 RA Kim T.-W., Wu K., Xu J.-L., McAuliffe G., Tanzi R.E., Wasco W.,
 RA Black I.B.;
 RT "Selective localization of amyloid precursor-like protein 1 in the
 RT cerebral cortex postsynaptic density.";
 RL Brain Res. Mol. Brain Res. 32:36-44(1995).
 RN [5]
 RP HEPARIN AND ZINC BINDING.
 RX MEDLINE=95014513; PubMed=7929392;

RA Bush A.I., Pettingell W.H. Jr., de Paradis M., Tanzi R.E., Wasco W.;
RT "The amyloid beta-protein precursor and its mammalian homologues.
RT Evidence for a zinc-modulated heparin-binding superfamily.";
RL J. Biol. Chem. 269:26618-26621(1994).

RN [6]

RP INTERACTION WITH APBA2.

RX MEDLINE=99107877; PubMed=9890987;

RA Tomita S., Ozaki T., Taru H., Oguchi S., Takeda S., Yagi Y.,
RA Sakiyama S., Kirino Y., Suzuki T.;

RT "Interaction of a neuron-specific protein containing PDZ domains with
RT Alzheimer's amyloid precursor protein.";

RL J. Biol. Chem. 274:2243-2254(1999).

RN [7]

RP EXTRACELLULAR COPPER-BINDING.

RX MEDLINE=22130992; PubMed=12135352;

RA Simons A., Ruppert T., Schmidt C., Schlicksupp A., Pipkorn R.,
RA Reed J., Masters C.L., White A.R., Cappai R., Beyreuther K.,
RA Bayer T.A., Multhaup G.;

RT "Evidence for a copper-binding superfamily of the amyloid precursor
RT protein.";

RL Biochemistry 41:9310-9320(2000).

CC -!- FUNCTION: May play a role in postsynaptic function. The C-terminal
CC gamma-secretase processed fragment, ALID1, activates transcription
CC activation through APBB1 (Fe65) binding (By similarity). Couples
CC to JIP signal transduction through C-terminal binding. May
CC interact with cellular G-protein signaling pathways. Can regulate
CC neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I.

CC -!- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
CC neuronal apoptosis (By similarity).

CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB and APBA family members,
CC MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its
CC serine phosphorylation (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
CC processed in the Golgi complex.

CC -!- TISSUE SPECIFICITY: Expressed in the cerebral cortex where it is
CC localized to the postsynaptic density (PSD).

CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The NPXY site is also involved in clathrin-mediated
CC endocytosis.

CC -!- PTM: Proteolytically cleaved by caspases during neuronal
CC apoptosis. Cleaved, in vitro, at Asp-620 by caspase-3 (By
CC similarity).

CC -!- PTM: N- and O-glycosylated.

CC -!- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
CC Zinc-binding increases heparin binding. No Cu(II) reducing
CC activity with copper-binding.

CC -!- SIMILARITY: Belongs to the APP family.

CC -----
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CC -----

DR EMBL; U48437; AAB96331.1; -.
DR EMBL; AD000864; AAB50173.1; -.
DR EMBL; BC012889; AAH12889.1; -.
DR HSSP; P05067; 1MWP.
DR Genew; HGNC:597; APLP1.
DR MIM; 104775; -.
DR GO; GO:0005604; C:basement membrane; TAS.
DR GO; GO:0007397; P:histogenesis and organogenesis; TAS.
DR GO; GO:0007399; P:neurogenesis; TAS.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KW Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
KW Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
KW Glycoprotein.
FT SIGNAL 1 38 POTENTIAL.
FT CHAIN 39 650 AMYLOID-LIKE PROTEIN 1.
FT CHAIN 621 650 C30 (BY SIMILARITY).
FT DOMAIN 39 580 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 581 603 POTENTIAL.
FT DOMAIN 604 650 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 158 178 COPPER-BINDING (BY SIMILARITY).
FT DOMAIN 204 211 ZINC-BINDING.
FT DOMAIN 310 342 HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN 410 441 HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN 442 459 COLLAGEN-BINDING (BY SIMILARITY).
FT DOMAIN 640 643 CLATHRIN-BINDING (POTENTIAL).
FT DOMAIN 241 247 POLY-GLU.
FT DOMAIN 264 268 POLY-GLU.
FT SITE 167 167 REQUIRED FOR COPPER(II) REDUCTION (BY
FT SIMILARITY).
FT SITE 604 615 BASOLATERAL SORTING SIGNAL (BY
FT SIMILARITY).
FT SITE 620 621 CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
FT SITE 638 641 ENDOCYTOSIS SIGNAL (BY SIMILARITY).
FT SITE 640 643 NPXY MOTIF.
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 551 551 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 48 48 A -> P (IN REF. 1).
SQ SEQUENCE 650 AA; 72176 MW; B95F0F4D1C5CBAC7 CRC64;

Query Match 28.6%; Score 1159.5; DB 1; Length 650;
Best Local Similarity 35.7%; Pred. No. 4.8e-51;
Matches 276; Conservative 114; Mismatches 229; Indels 155; Gaps 17;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
:| | || | :| :| | :| ||| :| :: |:|: || ::
Db 23 LLPLLLLLLLRAQPAIGSLAGGSPGAAEAPGSAQVAGLCGRLTLHRDLRTGRWEPDPQRSR 82

DE Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
 GN APLP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93066322; PubMed=1279693;
 RA Wasco W., Bupp K., Magendantz M., Gusella J.F., Tanzi R.E.,
 RA Solomon F.;
 RT "Identification of a mouse brain cDNA that encodes a protein related
 RT to the Alzheimer disease-associated amyloid beta protein precursor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP COLLAGEN-BINDING.
 RX MEDLINE=96139497; PubMed=8576160;
 RA Beher D., Hesse L., Masters C.L., Multhaup G.;
 RT "Regulation of amyloid protein precursor (APP) binding to collagen and
 RT mapping of the binding sites on APP and collagen type I.";
 RL J. Biol. Chem. 271:1613-1620(1996).
 RN [4]
 RP INTERACTION WITH DAB1.
 RX MEDLINE=99389880; PubMed=10460257;
 RA Homayouni R., Rice D.S., Sheldon M., Curran T.;
 RT "Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
 RT protein 1.";
 RL J. Neurosci. 19:7507-7515(1999).
 RN [5]
 RP INTERACTION WITH MAPK8IP1.
 RX MEDLINE=21408156; PubMed=11517249;
 RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,

RA Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,
 RA Kyriakis J.M., Nishimoto I.;
 RT "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1
 RT scaffolds Alzheimer's amyloid precursor protein with JNK.";
 RL J. Neurosci. 21:6597-6607(2001).
 RN [6]
 RP GAMMA-SECRETASE PROCESSING, INTERACTION WITH APBB1, AND MUTAGENESIS OF
 RP TYR-641.
 RX MEDLINE=22313598; PubMed=12228233;
 RA Scheinfeld M.H., Gherzi E., Laky K., Fowlkes B.J., D'Adamio L.;
 RT "Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-
 RT secretase regulates transcription.";
 RL J. Biol. Chem. 277:44195-44201(2002).
 CC -!- FUNCTION: May play a role in postsynaptic function. The C-terminal
 CC gamma-secretase processed fragment, ALID1, activates transcription
 CC activation through APBB1 (Fe65) binding. Couples to JIP signal
 CC transduction through C-terminal binding. May interact with
 CC cellular G-protein signaling pathways. Can regulate neurite
 CC outgrowth through binding to components of the extracellular
 CC matrix such as heparin and collagen I.
 CC -!- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
 CC neuronal apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB and APBA family members,
 CC MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its
 CC serine phosphorylation.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
 CC processed in the Golgi complex.
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The NPXY site is also involved in clathrin-mediated
 CC endocytosis.
 CC -!- PTM: Proteolytically cleaved by caspases during neuronal
 CC apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By
 CC similarity).
 CC -!- PTM: N- and O-glycosylated.
 CC -!- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
 CC Zinc-binding increases heparin binding. No Cu(II) reducing
 CC activity with copper-binding.
 CC -!- SIMILARITY: Belongs to the APP family.
 CC -----
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 CC -----
 DR EMBL; L04538; AAA37247.1; -.
 DR EMBL; BC021877; AAH21877.1; -.
 DR PIR; A46362; A46362.
 DR HSSP; P05067; 1MWP.
 DR MGD; MGI:88046; Aplp1.
 DR InterPro; IPR008155; A4_APP.

DR InterPro; IPR008154; A4_extra.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KW Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
KW Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
KW Glycoprotein.

FT	SIGNAL	1	37	POTENTIAL.
FT	CHAIN	38	653	AMYLOID-LIKE PROTEIN 1.
FT	CHAIN	624	653	C30 (BY SIMILARITY).
FT	DOMAIN	38	583	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	584	606	POTENTIAL.
FT	DOMAIN	607	653	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	157	177	COPPER-BINDING.
FT	DOMAIN	203	210	ZINC-BINDING (BY SIMILARITY).
FT	DOMAIN	313	345	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	413	444	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	445	462	COLLAGEN-BINDING (BY SIMILARITY).
FT	DOMAIN	263	271	POLY-GLU.
FT	DOMAIN	535	538	POLY-SER.
FT	DOMAIN	601	606	POLY-LEU.
FT	SITE	166	166	REQUIRED FOR COPPER(II) REDUCTION (BY
FT				SIMILARITY).
FT	SITE	607	618	BASOLATERAL SORTING SIGNAL (BY
FT				SIMILARITY).
FT	SITE	623	624	CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
FT	SITE	641	644	ENDOCYTOSIS SIGNAL.
FT	SITE	643	646	NPXY MOTIF.
FT	CARBOHYD	464	464	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	554	554	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	MUTAGEN	641	641	Y->G: REDUCED BINDING OF APBB1.
FT	CONFLICT	17	17	P -> PP (IN REF. 2).
SQ	SEQUENCE	653 AA;	72750 MW;	56516DC3EA40E4B0 CRC64;

Query Match 28.4%; Score 1150.5; DB 1; Length 653;
Best Local Similarity 35.4%; Pred. No. 1.4e-50;
Matches 274; Conservative 120; Mismatches 228; Indels 153; Gaps 19;

Qy	1	MLPGLALLLLAAWTARA-LEVPTDGNAGLLAEPQIAMFCGRLNMHNMNVQNGKWDSDPSGT	59
		: : : : : :: : : :	
Db	22	LLP-LSLLLLRAQLAVGNLAVGSPSAEAPGSAQVAGLCGRLTLHRDLRTGRWEPDPQRS	80
Qy	60	KTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHF-VIPYRCL	118
		: : : : : : : : : : : : :	
Db	81	RRCLLDPQRVLEYCRQMPYELHIARVEQAAQAI PMERWCGGTRSGRCAHPHHEVVPFHCL	140
Qy	119	VGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDK	178
		: : : : : : :	
Db	141	PGEFVSEALLVPEGCRFLHQERMDQCESSTRRHQEAQEACSSQGLILHGSGMLLPCGSDR	200
Qy	179	FRGVEFVCCPLAEESDNVDSADAEEDDSVW-WGGADTDYADGSEDKVVEVAEEEEVAEV	237
		: : : : :	
Db	201	FRGVEYVCCP-PPATPNPSGMAAGDPSTRSWPLGGR---AEGGED-----EEEVESF	248
Qy	238	EEEEADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEAET	297


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      : | : :| ||| || : |
Db    249 PQPVDDYFVEPPQAE EEEEEEEERAPPPSSHTP----- 281
Qy    298 GPCRAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPL 357
      |:|| ||
Db    282 ----VMVSR----VT----- 288
Qy    358 ARDPVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAE 417
      | || | || | ||: || | :|| || : :::||| || :
Db    289 ---PTPRPT-----DGVDVYFGMPGEIGEHEGFLRAKMDLEERRMRQINEVMREWAMAD 339
Qy    418 RQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYI 477
      |:|||||::|: :||| :::|:: : |||:|||| || |:|:| || ||| ::
Db    340 SQSKNLPKADRQALNEHFQSILQTL EEQVSGERQRLVETHATRVIALINDQRRAALEGFL 399
Qy    478 TALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVI 537
      ||| ||: | |:|:|||||::|:|:| |||:| | |:| || |||:| |
Db    400 AALQGDPPQAERVLMLRRYLRAEQKEQRHTLRHYQHVAAVDPEKAQQMRQVQVQTHLQVI 459
Qy    538 YERMNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDVLNMISEPRISYGNDALMP-S 596
      ||||| || | :|:|: : : ||| || : : || :| |
Db    460 EERMNQSLGLLDQNPHLAQELRPQIQELL-----LAEHLGPSEL----DASVPGS 505
Qy    597 LTETKTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGS 656
      :| | ||| |:::| | :| | : |
Db    506 SSEDK-----GSLQP-----PESKDDPPVTLP---KGSTDQESS 536
Qy    657 GLTNIKTEEISEVKMDAEFRHDSGYEVHH---QKLVFFAEDVGSNKGAIIGLMVGGVVIA 713
      | : : : | : | : | : : | : | : |
Db    537 SSGREKLTPLEQYEQKVNASAPRGFPFHSSDIQRDELAPSGTGVSREALSGLLIMGAGGG 596
Qy    714 TVIVITLVML-KKKQYTSIH HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQ 767
      ::||:|:|:| ||| | :| ||||| :| ||: | :::|:| |||||:| | :
Db    597 SLIVLSLLLLRKKKPYGTISHGVVEVDPM LTL EEQQLRELQRHGYENPTYRFLEE 651

```

RESULT 15

A4_CAEEL

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ID   A4_CAEEL          STANDARD;          PRT;    686 AA.
AC   Q10651; Q18583; Q95ZX1;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Beta-amyloid-like protein precursor.
GN   APL-1 OR C42D8.8.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE OF 6-686 FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=94089766; PubMed=8265668;
RA   Daigle I., Li C.;
RT   "apl-1, a Caenorhabditis elegans gene encoding a protein related to
RT   the human beta-amyloid protein precursor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:12045-12049(1993).

```



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RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Bristol N2;
RA      Hallsworth K.;
RL      Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN      [3]
RP      REVISIONS, AND ALTERNATIVE SPLICING.
RA      Waterston R.;
RL      Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
CC      -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC      -!- ALTERNATIVE PRODUCTS:
CC          Event=Alternative splicing; Named isoforms=2;
CC          Name=a;
CC              IsoId=Q10651-1; Sequence=Displayed;
CC          Name=b;
CC              IsoId=Q10651-2; Sequence=VSP_000017;
CC              Note=No experimental confirmation available;
CC      -!- SIMILARITY: Belongs to the APP family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U00240; AAC46470.1; ALT_INIT.
DR      EMBL; U56966; AAA98722.1; -.
DR      EMBL; U56966; AAK68242.1; -.
DR      PIR; T15795; T15795.
DR      HSSP; P05067; 1MWP.
DR      WormPep; C42D8.8a; CE04209.
DR      WormPep; C42D8.8b; CE27845.
DR      InterPro; IPR008155; A4_APP.
DR      InterPro; IPR008154; A4_extra.
DR      Pfam; PF02177; A4_EXTRA; 1.
DR      PRINTS; PR00203; AMYLOIDA4.
DR      SMART; SM00006; A4_EXTRA; 1.
DR      PROSITE; PS00319; A4_EXTRA; 1.
KW      Signal; Transmembrane; Amyloid; Neurogenesis; Glycoprotein;
KW      Alternative splicing.
FT      SIGNAL          1          21          POTENTIAL.
FT      CHAIN           22         686          BETA-AMYLOID-LIKE PROTEIN.
FT      DOMAIN          22         621          EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM        622         642          POTENTIAL.
FT      DOMAIN          643         686          CYTOPLASMIC (POTENTIAL).
FT      DOMAIN          205         228          ASP-RICH.
FT      DOMAIN          676         679          CLATHRIN-BINDING (POTENTIAL).
FT      CARBOHYD         84          84          N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD        201         201          N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD        249         249          N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD        417         417          N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      VARSPLIC        538         539          Missing (in isoform b).
FT                                          /FTId=VSP_000017.
SQ      SEQUENCE      686 AA;  79434 MW;  A0816858FDD48608 CRC64;

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Query Match 19.3%; Score 785; DB 1; Length 686;
Best Local Similarity 26.8%; Pred. No. 2.7e-32;
Matches 224; Conservative 111; Mismatches 272; Indels 230; Gaps 23;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK 60
      :: || : :| | | | | | | | | | | | | | | | | | | | | | | | | |
Db      6 LMIGLLIPILVA-TVYAEGSPAGSKRHEKFIPMVAFSCGYRNQYM-TEEGSWKTDDERYA 63

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      || | | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     64 TCFSGKLDILKYCRKAYPSMNITNIVEYSHEVSISDWCREEGSPCK-WTHSVRPYHCIDG 122

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTN-----LHDYGMLLPC 174
      || | :|| || | :| | | | : || | : | | : | : : :| ||
Db    123 EFHSEALQVPHDCQFSHVNSRDQCNDYQHWKDEAGKQCKTKKSKGNKDMIVRSAVLEPC 182

Qy    175 GIDKFRGVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEEV 234
      :| | ||||| | | :| : | : | : | : | : | : | : | : | : |
Db    183 ALDMFTGVEFVCCP-----NDQTNKTDVQKTK----- 209

Qy    235 AEVEEEEADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQ 294
      | :| : ||||| | : | | : :| ||
Db    210 ---EDEDDEDDDDAYEDDYSEESDEKDEE----- 236

Qy    295 AETGPCRAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQ 354
Db    237 ----- 236

Qy    355 EPLARDPVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWE 414
      || : :|| | : | | | | :| :| :| :| :| :| :| :| :| :| :|
Db    237 EPSSQDP-----YFKIANWTNEHDDFKKAEMRMDEKHKRKKVDKVMKEWG 280

Qy    415 EA-----ERQAKNLPKADKKAVIQ---HFQEKVESLEQEAANERQQLVETHMARVEAMLN 466
      : | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db    281 DLETRYNEQKAKD-PKGAEKFKSQMNARFQKTVSSLEEEHKRMRKEIEAVHEERVQAMLN 339

Qy    467 DRRRLALENYITAL--QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAA 524
      : : :| | :| || | | | | | :| :| :| :| :| :| :| :| :| :|
Db    340 EKKRDATHDYRQALATHVKNPKHSLVQSLKAYIRAEKDRMHTLNRYRHLLKADSKEAA 399

Qy    525 QIRSQVMTHLRVIYERMNQSLSLLYNVP-----AVA--EEIQDEVDELLOKEQNYS 573
      : | :| || | | :| :| :| :| :| | | : : :|| | : |
Db    400 AYKPTVIHRLRYIDLRINGTLAMLRDFPDLEKYVRPIAVTYWKDYRDEVSPDISVE---- 455

Qy    574 DDVLANMISEPRISYGN--DALMPSLT----ETKTTVELLPVNGEFSLDDLQPWHSFGAD 627
      | | :| : | | | :| | : | :| :| :| :| :| :| :| :| :|
Db    456 DSELTPIIHDDEFKNAKLDVKAPTTTAKPVKETDNAKVLPTASDSEEEADEYYEDED 515

Qy    628 SVPANT---ENEVEPVDARP-----AADRGLTTRPGSGLTNIKT 663
      | : :| :| || :| | | | | | | | | | | | | | | | | |
Db    516 EQVKKTPDMKKKVVDIKPKEIKVTIEEEKKAPKLVETSVQTDDEDDDEDSSSSTSES 575

Qy    664 EE-----ISEVKMDAE-----FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGG 709
      :| | | : :| | :|| | | :| | | :| :| :| :| :| :| :|
Db    576 DEDEDKNIKELRVDIEPIIDEPASFYRHD-----KLIQSPEVERSAASSVFQPYVLAS 627

Qy    710 VVIATVIVITLVMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFE 766
```

Db : | | | : | : | | | | | | | : : | | | | | | | | | :
628 AMFITAICIIAFAITNARRRRAMRGFIEVD-VYTPEERHVAGMQVNGYENPTYSFFD 683

Search completed: August 13, 2004, 09:13:17
Job time : 32.2051 secs